

85121 Text

Access DB#

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: SHIRLEY FRAY Examiner #: 2056 Date: 11/21/03
 Art Unit: 1608 Phone Number 30 8 3058 Serial Number: 1-10000002
 Mail Box and Bldg/Room Location: 812/6009 Results Format Preferred (circle): PAPER ☒ DISK ☐ E-MAIL ☐

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Self-Monitoring

Inventors (please provide full names): Robert L. ...

Earliest Priority Filing Date: 12/11/97

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

51d 50 is 50 alignments
these can be 100% (some are) 37q:
and any antibody that binds to any part of it 50 is 100%

May also include an interview with:

Please send to several Subscribers.

AK-2-379

BEST AVAILABLE COPY

STAFF USE ONLY

Searcher: D. S. L. 12-10-11

Searcher Phone #: 308-426-1111

Searcher Location: CM 6A03

Date Searcher Picked Up: _____

Date Completed: 1124103

Searcher Prep & Review Time: 30 / 3

Clerical Prep Time: _____

Online Time: 10 / 30

Type of Search

NA Sequence (#)_____

AA Sequence (#) 61

Structure (#) _____

Bibliographic _____

Litigation _____

Fulltext

Patent Family _____

Other _____

Vendors and cost where applicable

STN 12789

Dialog _____

Questel/Orbit _____

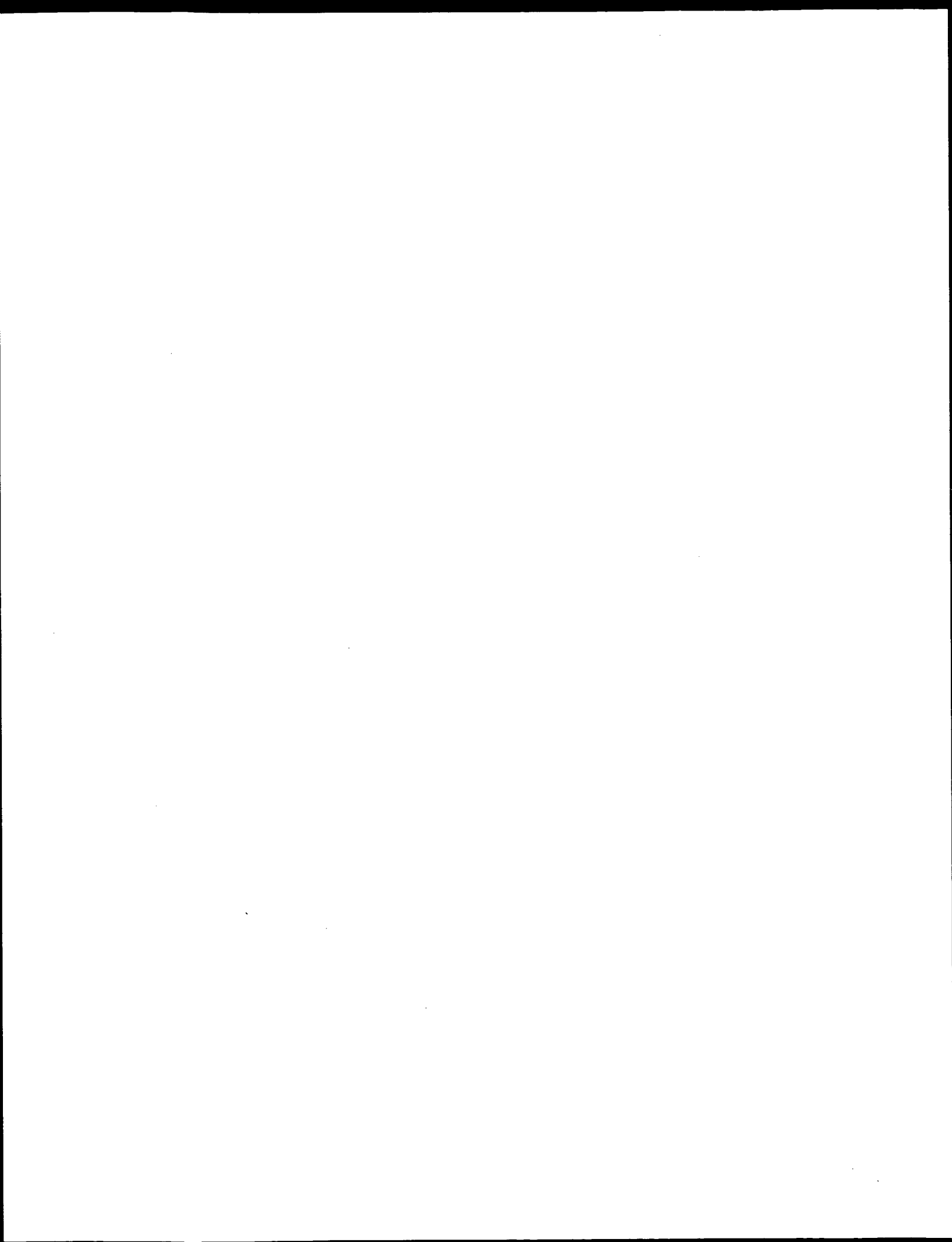
Dr. Link _____

Lexis/Nexis

Sequence Systems

WWW/Internet _____

Other (specify) _____



GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2003, 12:21:10 ; Search time 37 Seconds
(without alignments)
1364.919 Million cell updates/sec

Title: US-09-944-457-2

Perfect score: 1992

Sequence: 1 MKEVLLLLALCSAKPFFS.....PATFRCVLSRMSVQLGNFGM 379

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : A_Geneseq_101002.*
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22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1992	100.0	379	21	Human PRO241 polyp
2	1992	100.0	379	22	Human PRO241 polyp
3	1992	100.0	379	23	Human angiogenesis
4	1992	100.0	379	23	Human PRO241 prote
5	1990	99.9	379	20	Human PRO241 prote
6	1799	90.3	373	22	Mouse bone/cartila
7	1799	90.3	373	23	Murine protein iso
8	1649	82.8	344	22	Human polypeptide
9	1558	78.2	352	22	Novel human diagno
10	1237	62.1	245	22	Human protein sequ

11	1040.5	52.2	369	16	AAB87951	Rat neurotrophic b
12	1034	51.9	368	22	AAB85043	Human biglycan pro
13	1031.5	51.8	369	16	AAB87952	Human neurotrophic
14	1021	51.3	368	22	AAG78510	Human biglycan ami
15	1020	51.2	368	11	AAR05159	Sequence of human
16	1015	51.0	332	16	AAR87953	Bovine neurotroph
17	1007	50.6	197	22	AMA2137	Human polypeptide
18	963.5	48.4	359	21	AAV57079	Human decorin amin
19	963.5	48.4	359	22	AAV78511	Human decorin amin
20	963.5	48.4	360	22	AAU87286	Novel central nerv
21	949	47.6	342	17	AAR89439	Human recombinant
22	947	47.5	331	14	AAR42260	Mature decorin PT-
23	947	47.5	1388	17	AAR89471	Collagen/decorin f
24	947	47.5	1388	21	AAV84539	Amino acid sequenc
25	907	45.5	353	11	AAR05160	Sequence of human
26	847	42.5	305	14	AAR42267	Decorin sequence p
27	793.5	39.8	423	22	AAU30348	Novel human secret
28	776	39.0	280	14	AAR42266	Decorin sequence p
29	643	32.3	128	22	AAU20404	Human secreted pro
30	616	30.9	234	14	AAR42265	Decorin sequence p
31	493	24.7	88	21	AAG00241	Human secreted pro
32	493	24.7	88	21	AAV64720	Human 5' EST relat
33	493	24.7	186	14	AAR42264	Decorin sequence p
34	433	21.7	146	20	AAV59749	Human normal ovari
35	406.5	20.4	155	21	AB44116	Human cancer assoc
36	397.5	20.0	699	21	AAV67598	Human adipose tiss
37	393	19.7	353	21	AAB43535	Human cancer assoc
38	390	19.6	338	23	ABB90763	Human Tumour Endot
39	390	19.6	353	22	AAG73881	Human colon cancer
40	384.5	19.3	139	14	AAR42263	Decorin sequence p
41	366	18.4	421	20	AY05767	Human osteomodulin
42	366	18.4	421	21	AAB33417	Human PRO216 prote
43	366	18.4	421	21	AAB24435	Human PRO216 prote
44	366	18.4	421	21	AAV88377	PRO216 (osteomodul
45	366	18.4	421	22	AAU12322	Human PRO216 polyp
46	366	18.4	421	22	AB20340	Human PRO216. Hom
47	366	18.4	421	23	AAU81955	Human PRO216. Hom
48	366	18.4	772	22	ABB12438	Human bone marrow
49	363.5	18.2	674	22	AAW40226	Human polypeptide
50	363.5	18.2	674	22	AAU12189	Human PRO1483 poly

ALIGNMENTS

RESULT 1
AAB01311
ID AAB01311 standard; Protein; 379 AA.
AC AAB01311;
XX
XX 25-SEP-2000 (first entry)
DT
DE Human PRO241 polypeptide.
XX
XX PRO; membrane bound protein; secreted protein; PRO357; PRO327;
KW PRO243; PRO715; PRO241; PRO323; PRO299; PRO344; PRO347;
KW PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide;
KW antibody; screening; detection; inhibition; probe; primer; human.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Peptide 1..15 /label= Signal peptide
FT Modified-site 129..135 /note= "N-myristoylation site"
FT Domain 134..176 /label= Leucine zipper pattern
FT Modified-site 210..216 /note= "N-myristoylation site"
FT Modified-site 214..220 /note= "N-myristoylation site"

FT Modified-site 214..220
 FT /note= "N-myristoylation site"
 FT Modified-site 237..243
 FT /note= "N-myristoylation site"
 FT Modified-site 270..276
 FT /note= "N-myristoylation site"
 FT Modified-site 281..285
 FT /note= "N-glycosylation site"
 FT Modified-site 282..288
 FT /note= "N-myristoylation site"
 XX
 XX WO200032776-A2.
 PN
 XX
 XX 08-JUN-2000.
 XX
 XX 01-DEC-1999; 99WO-US28301.
 XX
 XX 01-DEC-1998; 98WO-US25108.
 XX 16-DEC-1998; 98US-0112850.
 XX 22-DEC-1998; 98US-0113296.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
 PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
 PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
 XX
 DR WPI: 2000-412324/35.
 DR N-PSDB: AAA49551.
 XX
 XX New human nucleic acids encoding secreted and transmembrane
 PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical
 PT and diagnostic agents
 XX
 PS Claim 12; Fig 2; 187pp; English.
 XX
 CC New human nucleic acids encoding secreted and transmembrane
 CC polypeptides which are designated as PRO polypeptides are described
 CC The membrane-bound proteins have various industrial applications,
 CC including as pharmaceutical and diagnostic agents. The membrane-bound
 CC proteins can also be employed for screening of potential peptide or
 CC small molecule inhibitors of the relevant receptor/ligand interaction.
 CC Anti-PRO antibodies are useful for the affinity purification of PRO
 CC from recombinant cell culture or natural sources.
 XX
 SQ Sequence 379 AA;
 Query Match 100.0%; Score 1992; DB 21; Length 379;
 Best Local Similarity 100.0%; Pred. No. 4e-177;
 Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKEYVLLFLALCSAKPFPSHIALKNMLKDMEDTDDDDDDDDDDDDNSLFPPTRE 60
 DB 1 MKEYVLLFLALCSAKPFPSHIALKNMLKDMEDTDDDDDDDDDDDDNSLFPPTRE 60
 QY 61 PRSHFFPDLPMCPFGCQYSRVHCSDGLTSVPTNIPDTRMLDLQNNKIKEIKEND 120
 DB 61 PRSHFFPDLPMCPFGCQYSRVHCSDGLTSVPTNIPDTRMLDLQNNKIKEIKEND 120
 QY 121 PKGLTSLGLIINNKKLTIIPKAFLLTKLRLYLSHNSQLSEIPLNPKSLAELRIHEN 180
 DB 121 PKGLTSLGLIINNKKLTIIPKAFLLTKLRLYLSHNSQLSEIPLNPKSLAELRIHEN 180
 QY 181 KYVKTKQDFTFGMALHVLKNSANPLDNNNGIEPGAFEGVTVFHRIAEAKLTSVPGKLGP 240
 DB 181 KYVKTKQDFTFGMALHVLKNSANPLDNNNGIEPGAFEGVTVFHRIAEAKLTSVPGKLGP 240
 QY 241 TLELHLDYNKISTVELDFRYKELQRLGLGNKNTDIENGSLANIIPRVREIHLNKKL 300
 DB 241 TLELHLDYNKISTVELDFRYKELQRLGLGNKNTDIENGSLANIIPRVREIHLNKKL 300
 QY 301 KKIPSGLPKELAYLOTIFLHNSIARVGVNDFCPTVPKMKKSLYSALSIFNNPVKYWEMOP 360
 DB 301 KKIPSGLPKELAYLOTIFLHNSIARVGVNDFCPTVPKMKKSLYSALSIFNNPVKYWEMOP 360

Db 301 KKIPSGLPKELAYLOTIFLHNSIARVGVNDFCPTVPKMKKSLYSALSIFNNPVKYWEMOP 360
 QY 361 ATFRCVLSRMSVOLGNFGM 379
 Db 361 ATFRCVLSRMSVOLGNFGM 379
 RESULT 2
 AAU12335
 ID AAU12335 standard; Protein; 379 AA.
 XX
 AC AAU12335;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human PRO241 polypeptide sequence.
 XX
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200140466-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 01-DEC-2000; 2000WO-US32678.
 XX
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 09-DEC-1999; 99US-0170262.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 30-DEC-1999; 99WO-US31243.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04342.
 PR 24-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 30-MAR-2000; 2000WO-US07532.
 PR 17-MAY-2000; 2000WO-US08439.
 PR 22-MAY-2000; 2000WO-US13705.
 PR 30-MAY-2000; 2000WO-US14042.
 PR 02-JUN-2000; 2000WO-US14941.
 PR 10-NOV-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI: 2001-408281/43.
 DR N-PSDB: AAS21407.
 XX
 XX Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical
 XX
 PS Claim 12; Fig 328; 813pp; English.

XX AAU12172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 XX

SQ Sequence 379 AA;

Query Match 100.0%; Score 1992; DB 22; Length 379;
 Best Local Similarity 100.0%; Pred. No. 4e-177;
 Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKEYVLLFLALCSAKPFPESHIALKNMMLKDMEDTDDDDDDDDDDDDSLFPFRE 60
 Db 1 MKEYVLLFLALCSAKPFPESHIALKNMMLKDMEDTDDDDDDDDDDDDSLFPFRE 60

QY 61 PRSHFFPDLPMCPFGCQCSRVVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKEND 120
 Db 61 PRSHFFPDLPMCPFGCQCSRVVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKEND 120

QY 121 FKGLTSLGLILNNKFKIHPKAFITTKLRRLYLSHNSQLSETPLNPKSLAELRIHEN 180
 Db 121 FKGLTSLGLILNNKFKIHPKAFITTKLRRLYLSHNSQLSETPLNPKSLAELRIHEN 180

QY 181 KYVKTKQDFTKGMALHVLMSANPLDNNNGIEPGAFESVTVFHIRIAEAKLTSVPKGLPP 240
 Db 181 KYVKTKQDFTKGMALHVLMSANPLDNNNGIEPGAFESVTVFHIRIAEAKLTSVPKGLPP 240

QY 241 TLELHLIDYKISTVELEDFRYKELQRLGLGNKKTIDIEGSLANIPRVREIHLNNKL 300
 Db 241 TLELHLIDYKISTVELEDFRYKELQRLGLGNKKTIDIEGSLANIPRVREIHLNNKL 300

QY 301 KKIPSGLPKLYLQIIFLHNSIARVGVNDFCPTVPKMKSLYSALISLNNPVKYMOP 360
 Db 301 KKIPSGLPKLYLQIIFLHNSIARVGVNDFCPTVPKMKSLYSALISLNNPVKYMOP 360

QY 361 ATRFCVLSRMSVQLGNFCM 379
 Db 361 ATRFCVLSRMSVQLGNFCM 379

RESULT 3
 ABB95437
 ID ABB95437 standard; Protein: 379 AA.
 XX AC ABB95437;
 XX 19-JUL-2002 (first entry)
 DE Human angiogenesis related protein PRO241 SEQ ID NO: 30.
 KW Human: angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiatic; cytosclerotic; antiangiogenic; hypotensive; vulnerary;
 XX antiarteriosclerotic.
 OS Homo sapiens.

XX PN WO200208284-A2.
 XX 31-JAN-2002.
 XX 09-JUL-2001; 2001WO-US21735.
 XX 20-JUL-2000; 2000US-219556P.
 XX 25-JUL-2000; 2000US-220624P.
 XX 25-JUL-2000; 2000US-220664P.
 XX 28-JUL-2000; 2000WO-US20710.
 XX 02-AUG-2000; 2000US-222695P.
 XX 17-AUG-2000; 2000US-0643657.
 XX 23-AUG-2000; 2000WO-US23522.
 XX 24-AUG-2000; 2000WO-US23328.
 XX 07-SEP-2000; 2000US-230978P.
 XX 15-SEP-2000; 2000US-000000P.
 XX 18-SEP-2000; 2000US-0664610.
 XX 18-SEP-2000; 2000US-0665350.
 XX 24-OCT-2000; 2000US-242922P.
 XX 08-NOV-2000; 2000US-0709238.
 XX 08-NOV-2000; 2000WO-US30952.
 XX 10-NOV-2000; 2000WO-US30873.
 XX 01-DEC-2000; 2000WO-US32678.
 XX 20-DEC-2000; 2000US-0747259.
 XX 20-DEC-2000; 2000WO-US34956.
 XX 22-JAN-2001; 2001US-0767609.
 XX 28-FEB-2001; 2001US-0796498.
 XX 28-FEB-2001; 2001WO-US06520.
 XX 01-MAR-2001; 2001WO-US06666.
 XX 09-MAR-2001; 2001US-0802706.
 XX 14-MAR-2001; 2001US-0808689.
 XX 22-MAR-2001; 2001US-0816744.
 XX 05-APR-2001; 2001US-0828366.
 XX 10-MAY-2001; 2001US-0854208.
 XX 10-MAY-2001; 2001US-0854280.
 XX 25-MAY-2001; 2001US-0866028.
 XX 25-MAY-2001; 2001US-0866034.
 XX 25-MAY-2001; 2001WO-US17092.
 XX 30-MAY-2001; 2001US-0870574.
 XX 30-MAY-2001; 2001WO-US17443.
 XX 01-JUN-2001; 2001WO-US17800.
 XX 20-JUN-2001; 2001WO-US19692.
 XX 28-JUN-2001; 2001WO-US00000.
 XX (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERK/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAONI/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI: 2002-171999/22.
 DR N-PSDB; ABL95575.
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX

Claim 11; Fig 30; 567pp; English.

The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention.

Sequence 379 AA;

Query Match 100.0%; Score 1992; DB 23; Length 379;
Best Local Similarity 100.0%; Pred. No. 4e-177;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPTR 60
Db 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPTR 60
QY 61 PRSHFFPDLFPMCPFGCQYSRVHVCSDGLTSVPTNIPFDRMLDLQNNKIKEIKEND 120
Db 61 PRSHFFPDLFPMCPFGCQYSRVHVCSDGLTSVPTNIPFDRMLDLQNNKIKEIKEND 120
QY 121 FKGLTSLYGLILNNKLTTHPKAFLTTKLRRLYLHSHNOLSEIPLNPKSLAELRIHEN 180
Db 121 FKGLTSLYGLILNNKLTTHPKAFLTTKLRRLYLHSHNOLSEIPLNPKSLAELRIHEN 180
QY 161 KVKIKQDFTFGMALHVLNSANPLDNGIEPCAFEGVTVFHIRIAEAKLTSVPKGLPP 240
Db 161 KVKIKQDFTFGMALHVLNSANPLDNGIEPCAFEGVTVFHIRIAEAKLTSVPKGLPP 240
QY 241 TLELHLDYNNKISTVELEDFKRYELQRLGLGNKKITDIENGSLANIPRVREIHLNNKL 300
Db 241 TLELHLDYNNKISTVELEDFKRYELQRLGLGNKKITDIENGSLANIPRVREIHLNNKL 300
QY 301 KKPISGLPELKYLIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSLFNNPVKYWMQ 360
Db 301 KKPISGLPELKYLIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSLFNNPVKYWMQ 360
QY 361 ATFRCLVLSRMSVQLGNFGM 379
Db 361 ATFRCLVLSRMSVQLGNFGM 379

RESULT 4
ABB84831
ID ABB84831 standard; Protein; 379 AA.

AC ABB84831;

DT 16-MAY-2002 (first entry)

DE Human PRO241 protein sequence SEQ ID NO:30.

KW Human: angiogenesis; cardiast; cytostatic; antiangiogenic; hypotensive;
KW vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping.

OS Homo sapiens.

PN WO200200690-A2.

PD 03-JAN-2002.

PF 20-JUN-2001; 2001WO-US19692.

PR 23-JUN-2000; 2000US-213637P.
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 30-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 01-JUN-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.

(GETH) GENENTECH INC.

Baker KP, Ferrara N, Gerber H, Gerecht ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

WPI: 2002-090516/12.

N-PSDB; ABL88086.

One hundred and eighty seven nucleic acids encoding PRO polypeptides,
useful in diagnosis and treatment of cardiovascular (e.g. myocardial
infarction), endothelial or angiogenic disorders in a mammal -

Claim 11; Fig 30; 565pp; English.

ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
ABB85003. The PRO proteins and polynucleotides have cardiac, cytostatic,
antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
activities, and can be used in gene therapy. The PRO polynucleotides,
proteins, agonists and antagonists are useful for treating or diagnosing
a cardiovascular, endothelial or angiogenic disorder in a mammal,
e.g. cardiac hypertrophy, trauma, cancer, age-related macular
degeneration, atherosclerosis, hypertension, arterial restenosis,
rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
carcinoma) and wound healing. The PRO polynucleotides have applications
in molecular biology, including use as hybridisation probes, and in
chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
probes used in the exemplification of the present invention.

Sequence 379 AA;

Query Match 100.0%; Score 1992; DB 23; Length 379;

Best Local Similarity 100.0%; Pred. No. 4e-177;

Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDNSLFPTR 60

XX	(GENE-) GENESTIS RES & DEV CORP LTD.
XX	Watson JD, Murison JG;
XX	WPI: 2001-425665/45.
XX	N-PDSB; AAD10114.
DR	
XX	Novel isolated polypeptide useful to isolate corresponding interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or other compounds, and as therapeutic target -
XX	Claim 6; Page 76-77; 101pp; English.
XX	The patent discloses novel polynucleotides and their corresponding proteins which play a major role in induction of growth, cell migration and proliferation, cell-cell interaction and the differentiation of tissue-specific cells. These proteins are important in the maintenance of tissue integrity and thus are important in wound healing. They are useful in various assays to determine the biological activity, to raise antibodies, to isolate corresponding interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or other compounds, and as therapeutic target in a whole range of disease states. Compositions comprising the novel proteins of the invention are useful for treating mammalian disorders. Polynucleotides of the invention are useful in genome and physical mapping, in positional cloning of genes, to tag or identify an organism or its reproductive material (as non-disruptive tags for marking organisms), and for the diagnosis and treatment of mammalian diseases which is the consequence of inappropriate expression of kinase genes. They are useful for promoting immune response as part of a vaccine or anti-cancer treatment, as target for cancer treatment, as immunoregulatory and anti-inflammatory molecule, as diagnostic for specific types of cancer and for development of an anti-cancer treatment, and as a target for antagonists in the treatment of diseases such as asthma and allergy. They are also useful to inhibit or enhance the activity of the soluble molecule that binds proteins of the invention, for tissue and neural regeneration, to promote or block cell trafficking, and as anti-inflammatory and/or vaccine adjuvant. The present sequence is bone/cartilage proteoglycan I (BGN) protein, a secreted protein from mouse. BGN is also known as biglycan or PG-SI.
XX	Sequence 373 AA;
SQ	
	Query Match 90.3%; Score 1799; DB 22; Length 373;
	Best Local Similarity 90.2%; Pred. No. 3.9e-159;
	Matches 341; Conservative 17; Mismatches 14; Indels 6; Gaps 1
QY	1 MKEYVLLFLALCSAKPFSPSHIALKNMKLKDMDTDDDDDDDDDEDNSLPFTR 60
Db	1 MKEYVMLLLAVCSAKPFSPSHTALKNMUKDMDTDDDDDDDD-----DNSLPTKE 54
QY	61 PRSHFFPDFLPMCPGCCYSRVVHCSDLGITSVPTNIPEDTMLDLNNKIKEIKEND 120 -
Db	55 PVNPFPDFLFTPCGCCOCYSRVVHSCDLGLTSVPNNIPEDTMVDLNNKIKEIKEND 114
QY	121 FKGLSLYLGLLNKKLTIKHPKAFETTKLRRLRYLSHNQLSEIPLNLPSKLAEIRHEN 180
Db	115 FKGLTSLYALLLNKKNTLIHKPELTFTTKLRRLRYLSHNQLSEIPLNLPSKLAEIRHDN 174
QY	181 KVKIKIDTFKGNNALHLVLEMSANPLDNNGTEPGAEGVTVFHIRIAEAKLTSVPKGLPP 240
Db	175 KVKIKIDTFKGNNALHLVLEMSANPLENGTEPGAEGVTVFHIRIAEAKLTSIPKGLPP 234
QY	241 TLLEHLNDYNKISTVELEDKFYKELQRLIGLGNKKITDIENGSLANTIPRRETHLENNKL 300
Db	235 TLLEHLDFNKISTVELEDKKRYRELQRGLGNRRITDIENGTANTIPRVRETHLEHNKL 294
QY	301 KKTPSGLPKLYLOIFLHSNRIARGVNDRCPTVPKMKSLSAISLFNNPKYWEWOP 360
Db	295 KKTPSGLQELKYLOIFLHNSIAKVGVNDRCPTVPKMKSLSAISLUFNNPMKIWEIQ 354
QY	361 ATFCVLRSMSVOLGNFG 378

QY 241 TLEHLDYKISTVELEDFKRYKELQRLGLGNKKTIDIEGSLANIPRVREIHLNKKL 300
 DB 235 TLEHLDYKISTVELEDFKRYKELQRLGLGNKKTIDIEGSLANIPRVREIHLNKKL 294
 QY 301 KKPISGLPELKYLIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSIFNNPVKYMEMP 360
 DB 295 KKPISGLPELKYLIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSIFNNPVKYMEMP 354
 QY 361 ATFRVLSRMSVQLGNFG 378
 DB 355 ATFRVLSRMSVQLGNVG 372

RESULT 8
 AAM40351
 ID AAM40351 standard; Protein: 344 AA.
 XX AC AAM40351;
 XX DT 22-OCT-2001 (first entry)
 XX DE Human polypeptide SEQ ID NO 3496.
 XX KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX OS Homo sapiens.
 XX PN WO200153312-A1.
 XX PD 26-JUL-2001.
 XX PF 26-DEC-2000; 2000WO-US34263.
 XX PR 21-JAN-2000; 2000US-0488725.
 XX PR 25-APR-2000; 2000US-052317.
 XX PR 09-JUL-2000; 2000US-0598042.
 XX PR 19-JUL-2000; 2000US-0620312.
 XX PR 03-AUG-2000; 2000US-0653450.
 XX PR 14-SEP-2000; 2000US-0662191.
 XX PR 19-OCT-2000; 2000US-0693036.
 XX PR 29-NOV-2000; 2000US-0727344.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX WPI; 2001-442253/47.
 XX N-PSDB; AAI59507.
 XX PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX Example 6; SEQ ID NO 3496; 10078pp; English.
 XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

XX Sequence 344 AA;

Query Match 82.8%; Score 1649; DB 22; Length 344;

Best Local Similarity 97.5%; Pred. No. 3.3e-145;

Matches 316; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 56 FPTPREPRSHFFPDLPMPGFCQCYSRVHCGSDGLTVPNTNIPDTRMLDQNNKIKE 115

DB 21 FQESQEAIFFPDLPMPGFCQCYSRVHCGSDGLTVPNTNIPDTRMLDQNNKIKE 80

QY 116 IKENDFKGLTSLYGLILNKKLTKIHPKAFITTKLRLRLYLSHNSLSEIPLNPKSLAE 175

DB 81 IKENDFKGLTSLYGLILNKKLTKIHPKAFITTKLRLRLYLSHNSLSEIPLNPKSLAE 140

QY 176 RIHENKVKIKQDFTFGMNAHVLEMSANPLDNNNGIEPGAFEGTVTFHIRIAEAKLTSVP 235

DB 141 RIHENKVKIKQDFTFGMNAHVLEMSANPLDNNNGIEPGAFEGTVTFHIRIAEAKLTSVP 200

QY 236 KGLPPTLLEHLDYKISTVELEDFKRYKELQRLGLGNKKTIDIEGSLANIPRVREIHL 295

DB 201 KGLPPTLLEHLDYKISTVELEDFKRYKELQRLGLGNKKTIDIEGSLANIPRVREIHL 260

QY 296 ENNKLKIPSGLPDELKYLIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSIFNNPVKY 355

DB 261 ENNKLKIPSGLPDELKYLIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSIFNNPVKY 320

QY 356 WEMQATFRVLSRMSVQLGNFGM 379

DB 321 WEMQATFRVLSRMSVQLGNFGM 344

RESULT 9

ABG22569

ID ABG22569 standard; Protein: 352 AA.

XX AC ABG22569;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #22560.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS86756.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX

3:

XX 02-JUN-1995; 95US-0458834.
 XX 14-NOV-1991; 91US-0792192.
 PR 17-NOV-1992; 92US-0978931.
 PR 08-SEP-1994; 94US-0303238.
 PR 28-JUN-1998; 88US-0212702.
 PR 22-JAN-1990; 90US-0467888.
 PR 13-MAY-1992; 92US-0882345.
 PA (BURN-) BURNHAM INST.
 XX Ruoslahti EI, Yamaguchi Y;
 PI WPI; 2001-610491/70.
 DR Use of decorin or biglycan polypeptide for inhibiting TGF-beta activity
 XX in the treatment of dermal wounds and cancer -
 PS Example 7; Fig 11; 40pp; English.
 XX The invention relates to the inhibition of transforming growth
 CC factor-beta (TGF-beta) activity involving contacting TGF-beta with a
 CC purified polypeptide comprising leucine-rich amino acid sequence of a
 CC member of decorin superfamily of mammalian proteoglycans. The following
 CC activities can be attributed to the polypeptide of the invention:
 CC cytostatic, nephrotropic, antirheumatic, antiarthritic, vasotropic,
 CC antiarteriosclerotic, hepatotropic, cardiant, dermatological and
 CC vulnerary. Polypeptides of the invention act as transforming growth
 CC factor-beta (TGF-beta) binder. The polypeptides of the invention can be
 CC used for treating a pathology, particularly proliferative pathology
 CC caused by a transforming growth factor-beta (TGF-beta) regulated
 CC activity such as cancer; particularly fibrotic cancer, fibrotic
 CC disease, glomerulonephritis, rheumatoid arthritis, arteriosclerosis,
 CC adult respiratory distress syndrome, cirrhosis of liver, fibrosis of
 CC lungs, post-myocardial infarction, cardiac fibrosis, post-angioplasty
 CC restenosis, renal interstitial fibrosis and certain dermal fibrotic
 CC conditions such as keloids and scarring resulting from burn injuries;
 CC other invasive skin injuries and reconstructive surgery. The wounds
 CC treated with the polypeptide, particularly decorin exhibit no detectable
 CC scarring, and are histologically normal. The current sequence represents
 CC human biglycan.
 XX Sequence 368 AA;
 SQ
 Query Match 51.3%; Score 1021; DB 22; Length 368;
 Best Local Similarity 52.4%; Pred. No. 1.3e-86;
 Matches 197; Conservative 64; Mismatches 95; Indels 20; Gaps 3;
 QY 6 LLLFLALCSAKPF-----FSPSHIALKNMMLKDMEDTDDDDDDDDDDDDSLFPTREP 61
 DB 7 LVSLALSQLALPFEQRGFWDFTLDDGPFMMNDEEASGADTSGVLDPD-----SVTPYTS- 60
 QY 62 RSHFFPFDLPMPFCQCYSRVVHCSDLGLTSVPTNIPEDTRMLDLQNNKIKEIKENDF 121
 DB 61 -----AMCPGCHLRVQVQSDGLKSVKPEISPTDTLLDLQNNDISELRKDDF 110
 QY 122 KGLTSLYGLIILNNKTKIHPKAFITTKKRLRYLSHNLSEIPLNLPKSLAELRIHENK 181
 DB 111 KGLQHLVALVLVNNKISKIHEKAFSPLRNVQKLYISKHNLVEIPLNLPSSLVLEIRHDNR 170
 QY 182 VKKIQKDTFGKGNALHVLMSANPLDNGIEPGAFEGVTVFHRIAEAKLTSPVKGLPPT 241
 DB 171 IRKVPNGVFSGLURNMNCIENGNGPLENSGFEFGAFDGLKLYLRISEAKLTGIPRDPET 230
 QY 242 LLEHLNDYKISTVELEDFKRYKELQRLGLGNKTTIDENGSLANIPRVREIHLNNKIK 301
 DB 231 LNELHLDHKNKIQAEIEDLLRYSKLYRLGLGHQIRMIENGSLFPLTLRELHLDNKKLA 290
 QY 302 KIPSGLPKLYLQITFLHSNSTARVGVNDPCTVPKMKKSLYSATISLFPNVPKYWEQPA 361
 DB 291 RVPSPGLPDLKLIQVYLLHSNNITKGVNDPFCPMGFGVKRAYNGISLFPNVPKYWEQPA 350

QY 362 TFRCVLSRMSVQLGNF 377
 DB 351 TFRCVTDRLAIQFGNY 366
 RESULT 15
 ID AAR05159
 XX AAR05159 standard; protein; 368 AA.
 AC AAR05159;
 XX 17-DEC-2001 (updated)
 DT 09-OCT-1990 (first entry)
 XX Sequence of human bone proteoglycan I (biglycan).
 DE Osteoporosis; rheumatoid arthritis; Paget's disease;
 KW atherosclerosis; periodontal; human bone matrix; proteoglycan.
 XX Homo sapiens.
 XX USN7432044-N.
 PN 17-APR-1990.
 PD 03-NOV-1989; 89US-0432044.
 XX 03-NOV-1989; 89US-0432044.
 PR (USSH) NAT INST OF HEALTH.
 PA Termine J;
 PI WPI; 1990-178641/23.
 DR N-PSDB; AAQ04490.
 XX Human bone matrix DNA and proteins -
 PT used in detection, diagnosis and treatment involving skeletal
 PT and/or connective tissue disease states.
 XX Disclosure; ; p; English.
 XX Probes and Abs raised to the proteins can be used to determine
 CC their levels useful in diagnosis of associated connective tissue
 CC diseases states such as osteoporosis, osteoarthritis, rheumatoid arthritis,
 CC Paget's disease, atherosclerosis and periodontal disease.
 CC Proteins may also be used to induce or block biological function.
 CC (Note: Revised entry submitted to correct the patent number format of
 CC US Government-owned NTIS applications to prevent clashes with ongoing US
 CC granted patent numbers. For further information please visit the Derwent
 CC web site at www.derwent.com/dwpl/updates/ntis_us.html.)
 XX Sequence 368 AA;
 SQ
 Query Match 51.2%; Score 1020; DB 11; Length 368;
 Best Local Similarity 52.1%; Pred. No. 1.6e-86;
 Matches 196; Conservative 66; Mismatches 94; Indels 20; Gaps 3;
 QY 6 LLLFLALCSAKPF-----FSPSHIALKNMMLKDMEDTDDDDDDDDDDDDSLFPTREP 61
 DB 7 LVSLALSQLALPFEQRGFWDFTLDDGPFMMNDEEASGADTSGVLDPD-----SVTPYTS- 60
 QY 62 RSHFFPFDLPMPFCQCYSRVVHCSDLGLTSVPTNIPEDTRMLDLQNNKIKEIKENDF 121
 DB 61 -----AMCPGCHLRVQVQSDGLKSVKPEISPTDTLLDLQNNDISELRKDDF 110
 QY 122 KGLTSLYGLIILNNKTKIHPKAFITTKKRLRYLSHNLSEIPLNLPKSLAELRIHENK 181
 DB 111 KGLQHLVALVLVNNKISKIHEKAFSPLRNVQKLYISKHNLVEIPLNLPSSLVLEIRHDNR 170
 QY 182 VKKIQKDTFGKGNALHVLMSANPLDNGIEPGAFEGVTVFHRIAEAKLTSPVKGLPPT 241
 DB 171 IRKVPNGVFSGLURNMNCIENGNGPLENSGFEFGAFDGLKLYLRISEAKLTGIPKDLPET 230

CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

XX Sequence 197 AA;
 CC Query Match 50.6%; Score 1007; DB 22; Length 197;
 CC Best Local Similarity 99.0%; Pred. No. 1.1e-85;
 CC Matches 191; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDT---DDDDDDDDDDDDDDSLPPT 58
 Db 3 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDSLPPT 62
 QY 59 REPRSHFFPDLPPMCPFGCQCYSRVHCSGLTSTVPTNIPDTRMLDLQNNKIKE 118
 Db 63 REPRSHFFPDLPPMCPFGCQCYSRVHCSGLTSTVPTNIPDTRMLDLQNNKIKE 122
 QY 119 NDFKGLTSLYGLTLNNKLTTHPKAFLTKKLRRLYLSHNLSEIPLNPKSLAELRIH 178
 Db 123 NDFKGLTSLYGLTLNNKLTTHPKAFLTKKLRRLYLSHNLSEIPLNPKSLAELRIH 182
 QY 179 ENKVKIKQDTEK 191
 Db 183 ENKVKIKQDTEK 195

RESULT 18
 AAY57079
 ID AAY57079 standard; protein; 359 AA.
 AC AAY57079;
 XX 28-FEB-2000 (first entry)
 XX Human decorin amino acid sequence.
 XX Neglected target tissue antigen; NNTA; autoimmunity; autoimmune response;
 KW immunotherapeutic agent; insulin dependent diabetes mellitus;
 KW multiple sclerosis; autoimmune thyroiditis; rheumatoid arthritis;
 KW uveoretinitis; inflammatory response.
 XX Homo sapiens.
 XX WO9556763-A1.
 XX 11-NOV-1999.
 XX 07-MAY-1999; 99WO-US10250.
 XX 07-MAY-1998; 98US-0084636.
 XX (REGC) UNIV CALIFORNIA.
 XX Kaufman DL, Tian J, Olcott A;
 XX WPI; 2000-052905/04.
 XX Administration of neglected target tissue antigens to modulate immune
 PT responses -
 XX Disclosure; Page 26; 79pp; English.

CC Amino acid sequences AAY57063-Y57091 are examples of neglected target
 CC tissue antigens NNTAs. NNTAs are antigens (whole antigens or fragments)
 CC not involved in autoimmunity. These peptides and proteins are used in
 CC the method of the invention which involves administering an NNTA as an
 CC antigen based immunotherapeutic agent, to a host afflicted with an
 CC autoimmune response associated with an autoimmune disease. The
 CC immunotherapeutic agent is used to treat autoimmune diseases such as
 CC insulin dependent diabetes mellitus, multiple sclerosis, autoimmune
 CC thyroiditis, uveoretinitis, rheumatoid arthritis or abnormal
 CC inflammatory immune responses. The NNTA induces regulatory tolerance by
 CC elicitation of regulatory T cells among T cells recognizing the NNTA but
 CC not participating in the immune response. The NNTA are capable of
 CC recognition by substantial populations of uncommitted T cells which can
 CC be primed, or biased, towards regulatory responses to provide effective
 CC treatment. The NNTA are effective in regulating undesirable immune
 CC responses even when target determinants used as agents promoting
 CC tolerance agents have failed to induce an effective regulatory T cell
 CC response. NNTAs as agents promoting tolerance are anticipated to be safer
 CC than use of target determinants.

XX Sequence 359 AA;
 CC Query Match 48.4%; Score 963.5; DB 21; Length 359;
 CC Best Local Similarity 50.4%; Pred. No. 2.9e-81;
 CC Matches 191; Conservative 65; Mismatches 100; Indels 23; Gaps 4;
 QY 1 MKEYVLLFLALCS-AKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDSLPPT 59
 Db 1 MKATITILLALQVSWAGPF---QORGLPDFMLEDEASGIGPEVDDR----- 45
 QY 60 EPRSHFFPDLPPMCPFGCQCYSRVHCSGLTSTVPTNIPDTRMLDLQNNKIKE 119
 Db 46 -----PEPSLGPVCPFRQCCHLRVVQCDLGLDKVPLDLPDPTLLDLQNNKITE 99
 QY 120 DFKGLTSLYGLTLNNKLTTHPKAFLTKKLRRLYLSHNLSEIPLNPKSLAELRIH 179
 Db 100 DFKNLKHLALILVNNKISKVSPGAFPLVKLRILYLSKNQKELPEKMPKTQLRAHE 159
 QY 180 NKVKIKQDTEKGMNALHLEMSANPLDNGNIEGAFEGV-TVPHIRTAELKSLVPGKL 238
 Db 160 NEITKVRKVTFTNGLNQMTIVIELGTNPLKSSGIEGAFQGMKKLSYIRIADTNITSPOGL 219
 QY 239 PPTLELHLDYNNKISTVELEDFKRYKELQRLGLGNKLTIDENGSLANIPRVRETHLENN 298
 Db 220 PPSLTELHLDGNKISRVDAAASLKGLNLAKLGLSFNSISAVDNGSLANTPHRLHLDNN 279
 QY 299 KLKIPSGELPELKYLIIFLHNSIARVGVNDFCTVPKMKKSLYSALSLENNPVKWE 358
 Db 280 KLTRVPGGLAEHKYIQVYVYLNHNINISVVGSSDFCPCPGHNTKKASVGSVLSFNPVYWEI 339
 QY 359 QPATERCVLSRMSVOLGNF 377
 Db 340 QPATERCVYVRSAILQGNV 358

RESULT 19
 AAG78511
 ID AAG78511 standard; protein; 359 AA.
 AC AAG78511;
 XX 29-JAN-2002 (first entry)
 XX Human decorin amino acid sequence.
 XX Fibromodulin; Decorin; Biglycan; Proteoglycan; Extracellular matrix;
 KW TGF-beta; Transforming growth factor-beta; Burn; Wound; Cytostatic;
 KW Nephrotropic; Antirheumatic; Antiarthritic; Vasotropic; Vulnary
 KW Antiartherosclerotic; Hepatotropic; Cardiant; Dermatological;
 KW Glomerulonephritis; Rheumatoid arthritis; Arteriosclerosis;
 KW Adult respiratory distress syndrome; Cirrhosis; Cancer; Fibrotic.
 XX Homo sapiens.

PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226860.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 08-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231960.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.

PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 03-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 PI
 XX WPI; 2001-581633/65.
 DR N-PSDB; ABK43616.
 DR
 XX
 PT New Isolated nucleic acid encoding a protein for diagnosing,
 PT preventing, treating or ameliorating medical conditions and used as
 PT food additives or preservatives -
 XX
 PS Claim 9; SEQ ID No 804; 837pp; English.

XX The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical condition and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amyotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, CC

Query Match 48.4%; Score 963.5; DB 22; Length 360;

ID AAY84539 standard; Protein; 1388 AA.
 XX AAY84539;
 AC
 XX 25-JUL-2000 (first entry)
 DT
 XX Amino acid sequence of a chimeric collagen 1 (alpha1)/decorin protein.
 DE
 XX Extracellular matrix protein; self aggregation; hydroxylated proline;
 KW trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production;
 KW collagen; fibrinogen; fibronectin; post translational hydroxylation;
 KW decorin; chimera.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 87 /note= "Gly encoded by GCG"
 FT Misc-difference 305 /note= "Glu encoded by CAA"
 FT Misc-difference 363 /note= "Gly encoded by CGT"
 FT Misc-difference 378 /note= "Glu encoded by GGT"
 FT Misc-difference 429 /note= "Gly encoded by CGA"
 FT Misc-difference 444 /note= "Gly encoded by GCG"
 FT Misc-difference 543 /note= "Gly encoded by GCG"
 FT Misc-difference 546 /note= "Gly encoded by GCT"
 FT Misc-difference 606 /note= "Gly encoded by GAC"
 FT Misc-difference 702 /note= "Gly encoded by GCG"
 FT Misc-difference 815 /note= "Pro encoded by CTT"
 FT Misc-difference 858 /note= "Gly encoded by GCT"
 FT Misc-difference 1066 /note= "Gly encoded by GCC"
 FT
 XX EF992586-A2.
 PN
 XX 12-APR-2000.
 PD
 XX 07-OCT-1999; 99EP-0119184.
 PF
 XX 09-OCT-1998; 98US-0169768.
 PR
 XX (USSU) US SURGICAL CORP.
 PA
 XX Gruskin EA, Buechter DD, Zhang G, Connolly K;
 PI
 XX WPI; 2000-259138/23.
 XX N-PSDB; AAA12499.
 DR
 XX Production of extracellular matrix proteins containing
 PT 4-trans-hydroxyproline results in native self aggregating proteins,
 FT useful on medical implants -
 FT
 XX Claim 25; Fig 17A-B; 260pp; English.
 PS
 XX The specification describes a method for producing an extracellular
 CC matrix protein or its fragment. The extracellular matrix protein is
 CC capable of self aggregating in a cell which does not ordinarily
 CC hydroxylated prolines. The method comprises optimising a nucleic acid
 CC sequence for expression in the cell by substitution of codons preferred
 CC by that cell for naturally occurring codons not preferred by the cell;
 CC incorporating the nucleic acid sequence into the cell; and contacting
 CC the cell with a hypertonic growth medium containing at least one amino

CC acid, selected from the group consisting of trans-4-hydroxyproline and
 CC 3-hydroxyproline to allow at least one of the amino acids to be
 CC assimilated into the cell and incorporated into the extracellular matrix
 CC protein. The method may be used to make host cells assimilate and
 CC incorporate trans-4-hydroxyproline into proteins. This is especially
 CC useful in the recombinant production of proteins such as collagen,
 CC fibrinogen and fibronectin whose ability to self aggregate and produce
 CC functional proteins depends on the post translational hydroxylation of
 CC proline. The method is also useful in studying the structure and function
 CC of polypeptides which do not normally contain trans-4-hydroxyproline.
 CC The present sequence represents a chimeric collagen 1 (alpha1)/decorin
 CC protein, which may be produced using the method of the invention.
 XX
 SQ Sequence 1388 AA;
 Query Match 47.5%; Score 947; DB 21; Length 1388;
 Best Local Similarity 54.1%; Pred. No. 6.6e-79;
 Matches 178; Conservative 62; Mismatches 87; Indels 2; Gaps 2;
 QY 50 DDNSLFTPTREPRSHFFDFPMGFCQCYSRVVHCSDLGLTSVPTNIPDFTRMLDLQ 109
 DB 1060 DEASGIGP-EVPDDRDFEPLSLGVPVCPFCQCHLRVVCQSDGLDKVPKDLPTLLDLQ 1118
 QY 110 NKKIKIENDEKGLTSLYGLILANNKLTHTPKAFLTTKKLRRLYLHNSNLSSEIPNL 169
 DB 1119 NKKITEIKDGFKNLKNLHALILVNNKISKVSGAFTPLVKRLYLKSNOLKELPEKMP 1178
 QY 170 KSLAELRIHENKVKKIOKDTFGMNAHLVLEMSANPLDNGNGIEPGAFEGV-TVFHRIAE 228
 DB 1179 KTLQELRAHENEITKRVKVTENGLOMIVIELGTNPLKSSGIENGAFOMKKLSYRIAD 1238
 QY 229 AKLTSVPKGLPPTLLEHLHDYNNKISTVELEDFKRYKELQRLGLGNKKTIDENGLANIP 288
 DB 1239 TNITSIPOGLPPLTELHLDGNNKISRVDAAALIKLNNLAKLGLSFNSISAYDNGSLANTP 1298
 QY 289 RVREIHLNENKLTPTSGLPKLYLOIIFLHNSNISTARVGVNDFCTVPKMKKSLYSATSL 348
 DB 1299 HLREHLNENKLTPTSGLPKLYLOIIFLHNSNISTARVGVNDFCTVPKMKKSLYSATSL 1358
 QY 349 FNNPVKYMOPATPCVLSRMSVOLGNF 377
 DB 1359 FSNPVQWEIQPSTFCVVRSAIOLGNV 1387
 RESULT 25
 AAR05160 standard; protein; 353 AA.
 ID AAR05160
 XX
 AC AAR05160;
 DT 17-DEC-2001 (updated)
 DT 09-OCT-1990 (first entry)
 XX
 DE Sequence of human bone proteoglycan II (decorin).
 KW Osteoporosis; rheumatoid arthritis; Paget's disease;
 KW atherosclerosis; periodontal; human bone matrix; proteoglycan.
 XX
 OS Homo sapiens.
 XX
 PN USN7432044-N.
 XX
 PD 17-APR-1990.
 PF 03-NOV-1989; 89US-0432044.
 PR 03-NOV-1989; 89US-0432044.
 XX (USSH) NAT INST OF HEALTH.
 XX Termine J;
 XX WPI; 1990-178641/23.
 DR

06-DEC-2001 (first entry)
 Human secreted protein, Seq ID No 396.
 Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina; rheumatoid arthritis; antiarteriosclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmological; cytostatic; Alzheimer's disease; Parkinson's disease; human; multiple sclerosis; cancer; hyperproliferative disorder; infection; Gaucher's disease; neurological disease; cerebrovascular disorder; thrombosis; wound healing.
 Homo sapiens.
 WO200155326-A2.
 02-AUG-2001.
 17-JAN-2001; 2001WO-US01347.
 31-JAN-2000; 2000US-0179065.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-451931/48.
 N-PSDB; AAS33113.
 New nucleic acids and polypeptides, useful for diagnosing, preventing or treating medical conditions -
 Claim 11; SEQ ID No 396; 753pp; English.
 The invention relates to novel isolated nucleic acid molecules (I) encoding human secreted proteins (II). (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate expression of secreted proteins. (I) and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and so which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of the secreted proteins. The anti-(II) antibodies and antagonists may also be used to down regulate expression and activity of (II). The anti-(II) antibodies may also be used as diagnostic agents for detecting the presence of (II) in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease and Charcot-Marie-Tooth disease), cardio-/cerebrovascular disorders (e.g. cardiac arrest, tachycardia, angina and thrombosis), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). (I) and (II), agonists, antagonists and antibodies can also be used to promote wound healing, maintain organs before transplantation, and support cell culture of primary tissues. AAU20342-AAU20666 represent human secreted protein amino acid sequences, and related sequences of the invention.
 Note: The sequence data for this patent did not appear in the printed specification but was obtained in electronic format directly from WIPO at: ftp.wipo.int/pub/published_pct_sequences.
 Sequence 128 AA;

Query Match 32.3%; Score 643; DB 22; Length 128;
 Best Local Similarity 98.4%; Pred. No. 5.2e-55;
 Matches 125; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 253 STVELEDFKRYKELQRLGLGNKNTDIENGLANIPIVREIHLNNKIKIPSGLPKLY 312
 Db 2 STVELEDKRXKELQRLGLGNKNTDIENGLANIPIVREIHLNNKIKIPSGLPKLY 61
 QY 313 LQIIFLHNSNISTARVGVNDFCTVTPKMKKSLYSALSIFNNPVKYWEMOPATFRCVLSRMSV 372
 Db 62 LQIIFLHNSNISTARVGVNDFCTVTPKMKKSLYSALSIFNNPVKYWEMOPATFRCVLSRMSV 121
 QY 373 QLGNFGM 379
 Db 122 QLGNFGM 128
 RESULT 30
 AAR42265
 ID AAR42265 standard; Protein; 234 AA.
 XX
 AC AAR42265;
 XX
 DT 28-APR-1994 (first entry)
 XX
 DE Decorin sequence PT-76 (N-terminal to LRR8).
 XX
 KW leucine-rich repeat; proteoglycan; cell regulatory factor; MBP;
 KW fusion protein; maltose binding protein; tumour growth; inhibition;
 KW decorin; PG-II; PG-40; transforming growth factor-beta; TGF-beta.
 XX
 PN WO9320202-A.
 XX
 PD 14-OCT-1993.
 XX
 PF 02-APR-1993; 93WO-US03171.
 XX
 PR 03-APR-1992; 92US-0865652.
 XX
 PA (LJOL-) LA JOLLA CANCER RES FOUND.
 XX
 PI Cardenas J, Craig W, Mullen DG, Pierschbacher MD;
 PI Ruoslahti EI;
 DR WPI; 1993-336910/42.
 DR N-PSDB; AAQ50051.
 XX
 PT Active fragments of protein esp. decorin - with cell regulatory
 PT factor domain, useful for inhibiting cell regulatory factor
 PT activity
 XX
 PS Claim 10; Page 45-46; 77pp; English.
 XX
 PS Active fragments of decorin (full-length coding sequence AAQ50046)
 CC were generated by PCR and fused to Maltose Binding Protein. The
 CC resulting fusion proteins were useful for inhibiting the activity of
 CC a cell regulatory factor, esp. TGF-beta, and hence for treating
 CC conditions associated with over-activity of the growth factor such
 CC as certain tumours.
 XX
 SQ Sequence 234 AA;
 Query Match 30.9%; Score 616; DB 14; Length 234;
 Best Local Similarity 52.4%; Pred. No. 4e-49;
 Matches 122; Conservative 40; Mismatches 69; Indels 2; Gaps 2;
 QY 50 DEONSLFFTEPRSHFPFDFLFWCPCFGCCYRVVHCSDLGLTSYPTNIPFTRMLDLQ 109
 Db 3 DEASGIGP-EVPDRDFPESLGVPCFRCOCHLRVQCSDGLDKVCKDLPDPTTLLDLQ 61
 QY 110 NNRKIKENDFKGLTSLYGLILNNKLTIKHPKAFLTTKRLRLYLHSHNOLSEIFLNLP 169
 Db 62 NNRKIKENDFKGLTSLYGLILNNKLTIKHPKAFLTTKRLRLYLHSHNOLSEIFLNLP 121
 QY 170 KSLAELRIHENKVKYKIOKDTFKGMNALHLEMSANLNDNNGIEPGAFEGV-TVFHIRIAE 228
 Db 122 KTLQELRAHENEITKVRKVTFTNGLNQMVIELGTNPLKSSGIENGAFQGMKLSYRIAD 181

Db	680	YTFSCIRSYSSIVL 693	
RESULT 37			
AAB43535			
ID	AAB43535	standard; Protein; 353 AA.	
XX			
AC	AAB43535;		
XX			
DT	08-FEB-2001	(first entry)	
XX			
DE	Human cancer associated protein sequence SEQ ID NO:980.		
XX			
KW	Human; cancer associated gene; cancer antigen; detection; cancer;		
KW	diagnosis; cytostatic; proliferative; vulnerable; immunomodulator;		
KW	antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;		
KW	antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;		
KW	dermatological; neuroprotective; thrombolytic; coagulant; nootropic;		
KW	vasotopic; antipsoriatic; antiangiogenic; gene therapy; inflammation;		
KW	immune disorder; haematopoietic cell disorder; autoimmune disorder;		
KW	allergic reaction; graft versus host disease; organ rejection;		
KW	haemostatic; thrombolytic; cardiovascular disorder; infection;		
KW	neurological disease; drug screening.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200055350-A1.		
XX			
PD	21-SEP-2000.		
XX			
PF	08-MAR-2000; 2000WO-US05882.		
XX			
PR	12-MAR-1999; 99US-0124270.		
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		
PI	Rosen CA, Ruben SM;		
XX			
DR	WPI; 2000-587533/55.		
DR	N-PSDB; AAC77744.		
XX			
PT	Novel isolated nucleic acids comprising sequences encoding peptides		
PT	useful for treating or diagnosing e.g. cancer -		
XX			
PS	Claim 11; Page 1552-1553; 2352pp; English.		
XX			
CC	AAC77607 to AAC78448 encode the human cancer associated proteins given		
CC	in AAB43398 to AAB44239. The proteins can have activities based on the		
CC	tissues and cells the genes are expressed in. Example of activities		
CC	include: cytostatic; proliferative; vulnerable; immunomodulator;		
CC	antidiabetic; antiasthmatic; antirheumatic; antiarthritic;		
CC	antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;		
CC	dermatological; neuroprotective; cardiant; thrombolytic; coagulant;		
CC	nootropic; vasotopic; antipsoriatic and antiangiogenic. The		
CC	polynucleotides and polypeptides can be used for preventing, treating or		
CC	ameliorating medical conditions and diagnosing pathological conditions.		
CC	Polynucleotides, polypeptides, antibodies, agonists and antagonists from		
CC	the present invention may be used to treat immune disorders by activating		
CC	or inhibiting the proliferation, differentiation or mobilisation of		
CC	immune cells, to treat disorders of haematopoietic cells, autoimmune		
CC	disorders, allergic reactions, graft versus host disease and organ		
CC	rejection, modulate haemostatic or thrombolytic activity, modulate		
CC	inflammation, cancers, cardiovascular disorders, neurological disease and		
CC	bacterial or viral infections. The peptides, nucleotides, antibodies,		
CC	agonists and antagonists may be also be used in drug screens AAC78449 to		
CC	AAC78457 and AAB44240 represent sequences used in the exemplification of		
CC	the present invention.		
XX			
SQ	Sequence 353 AA;		
Query Match	19.7%; Score 393; DB 21; Length 353;		
Best Local Similarity	31.7%; Pred No. 4.3e-28;		
Matches 102; Conservative	70; Mismatches 128; Indels 22; Gaps 10;		

CC subjects bearing a vascularised tumour, polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
 CC and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
 CC ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
 CC sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and
 CC ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
 CC and pan-endothelial markers (PEM) ABL91903-ABL91995.
 XX
 SQ Sequence 338 AA;
 Query Match 19.6%; Score 390; DB 23; Length 338;
 Best Local Similarity 31.8%; Pred. No. 7.8e-28;
 Matches 100; Conservative 70; Mismatches 122; Indels 22; Gaps 10;
 Qy 66 FPDLEF---PWCDFGQCQ---YSRVHCSDLGLTSVPTNIPEDTRMLDQNNKIKEIKE 118
 Db 25 FPLSTYGQSSPNCAPCEPCPSYAMCYDELKLSVPM-VPPGKLYLYLRNQIDHIDE 83
 Qy 119 NDFKGLTSLYGLILNNKLL--TKIHPKAFLTTKLRRLYLHSHNOLSEIPLNPKSLAELR 176
 Db 84 KAFENVDTQLWLIDHNLNLSKIKGRVFSKQLKQLKHLHNNHNLTSVGLPKSLEDLQ 143
 Qy 177 IHENKVKKIQTDFKGMNALHVLMSANPLDNNNGIEPGAFEGV-TVFHRIAEAKLTSVP 235
 Db 144 LTHNKITKL--GSFEGVLNLTFIHQHNLKEDAVS-AAFKGLKSLLEYLDLSFNQIARLP 200
 Qy 236 KGLPPTLELHLDYKNISTVELEDFKRYKELQRLGLGNKKTIDIE-NGSLANIPRVREIH 294
 Db 201 SGLPVSLLTLYLDNNKISNIPDEYFKRFNALQYLRSHNELADSGIPGNSFVSSLVELD 260
 Qy 295 LENNKKKIPSGLPPELK--YLIQIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSIFNFP 352
 Db 261 LSYNKLKNIPTVNELENYILEV-----NQLEKFDIKSFCKILGPLSYSKIKHLRLDGNR 315
 Qy 353 VKYWEQAPATRCV 366
 Db 316 ISETSLPPDMYECL 329
 RESULT 39
 AAG73881
 ID AAG73881 standard; Protein; 353 AA.
 AC AAG73881;
 XX
 DT 03-SEP-2001 (first entry)
 XX
 DE Human colon cancer antigen protein SEQ ID NO:4645.
 XX
 KW Human; colon cancer; colon cancer antigen; diagnosis: detection;
 KW colorectal carcinoma; chromosome 12.
 XX
 OS Homo sapiens.
 XX
 PN WO200122920-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 28-SEP-2000; 2000WO-US26524.
 XX
 PR 29-SEP-1999; 99US-0157137.
 PR 03-NOV-1999; 99US-0163280.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ruben SM, Barash SC, Birse CE, Rosen CA;
 XX WPI; 2001-235357/24.
 DR N-PSDB; AAB33312.
 XX
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers -

PS
 XX Claim 11; Page 6448-6450; 9803pp; English.
 CC AAB32943 to AAB37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the patients own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated Ps,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAB37196 to AAB37204
 CC and AAB7789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.
 XX
 SQ Sequence 353 AA;
 Query Match 19.6%; Score 390; DB 22; Length 353;
 Best Local Similarity 31.8%; Pred. No. 8.3e-28;
 Matches 100; Conservative 70; Mismatches 122; Indels 22; Gaps 10;
 Qy 66 FPDLEF---PWCDFGQCQ---YSRVHCSDLGLTSVPTNIPEDTRMLDQNNKIKEIKE 118
 Db 40 FPLSTYGQSSPNCAPCEPCPSYAMCYDELKLSVPM-VPPGKLYLYLRNQIDHIDE 98
 Qy 119 NDFKGLTSLYGLILNNKLL--TKIHPKAFLTTKLRRLYLHSHNOLSEIPLNPKSLAELR 176
 Db 99 KAFENVDTQLWLIDHNLNLSKIKGRVFSKQLKQLKHLHNNHNLTSVGLPKSLEDLQ 158
 Qy 177 IHENKVKKIQTDFKGMNALHVLMSANPLDNNNGIEPGAFEGV-TVFHRIAEAKLTSVP 235
 Db 159 LTHNKITKL--GSFEGVLNLTFIHQHNLKEDAVS-AAFKGLKSLLEYLDLSFNQIARLP 215
 Qy 236 KGLPPTLELHLDYKNISTVELEDFKRYKELQRLGLGNKKTIDIE-NGSLANIPRVREIH 294
 Db 216 SGLPVSLLTLYLDNNKISNIPDEYFKRFNALQYLRSHNELADSGIPGNSFVSSLVELD 275
 Qy 295 LENNKKKIPSGLPPELK--YLIQIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSIFNFP 352
 Db 276 LSYNKLKNIPTVNELENYILEV-----NQLEKFDIKSFCKILGPLSYSKIKHLRLDGNR 330
 Qy 353 VKYWEQAPATRCV 366
 Db 331 ISETSLPPDMYECL 344
 RESULT 40
 AAR42263
 ID AAR42263 standard; Protein; 139 AA.
 XX
 AC AAR42263;
 XX
 DT 28-APR-1994 (first entry)
 XX
 DE Decorin sequence PT-74 (N-terminal to LRR4).
 XX
 KW leucine-rich repeat; proteoglycan; cell regulatory factor; MBP;
 KW fusion protein; maltose binding protein; tumour growth; inhibition;
 KW decorin; PG-II; PG-40; transforming growth factor-beta; TGF-beta.
 XX
 PN WO9320202-A.
 XX
 PD 14-OCT-1993.
 XX
 PF 02-APR-1993; 93WO-US03171.
 XX

PR 03-APR-1992; 92US-0865652.
 XX (LJOL-) LA JOLLA CANCER RES FOUND.
 PA Cardenas J, Craig W, Mullen DG, Pierschbacher MD;
 PI Ruoslahti EI;
 XX WPI; 1993-336910/42.
 DR N-PSDB; AAO50049.
 XX
 PT Active fragments of protein esp. decorin - with cell regulatory
 PT factor domain, useful for inhibiting cell regulatory factor
 XX activity
 PS Claim 10; Page 41; 77pp; English.
 XX
 CC Active fragments of decorin (full-length coding sequence AAO50046)
 CC were generated by PCR and fused to Maltose Binding Protein. The
 CC resulting fusion proteins were useful for inhibiting the activity of
 CC a cell regulatory factor, esp. TGF-beta, and hence for treating
 CC conditions associated with over-activity of the growth factor such
 CC as certain tumours.
 XX
 SQ Sequence 139 AA;
 Query Match 19.3%; Score 384.5; DB 14; Length 139;
 Best Local Similarity 55.1%; Pred. No. 7.3e-28;
 Matches 76; Conservative 20; Mismatches 41; Indels 1; Gaps 1;
 QY 50 DDNSLFTTREPSSHFFPDLFPMCPGCGCYSRVHCSDGLTSVPTNIPFDTRMLDLQ 109
 Db 3 DEASIGP-EVPDDRDFEPLSGVPCFRCQCHLRVQCSDLGLDKVPKDLPPDTTLLDLQ 61
 QY 110 NKKIKEIKENDKGLTSLYGLLNNKLTHTPKAFLLTKLRRLYLSHNSLSEIPLNLP 169
 Db 62 NKKITEIKDGFKNLKNHALILVNNKLSVSPGAFPLVKLERLYLSKNQKELPEKMP 121
 QY 170 KSLAELRIHENVKVKIQK 187
 Db 122 KTLQELRAHENEITKVRK 139
 RESULT 41
 AAY05767
 ID AAY05767 standard; Protein; 421 AA.
 XX
 AC AAY05767;
 XX
 DT 19-JUL-1999 (first entry)
 XX
 DE Human osteomodulin PRO216.
 XX
 KW Osteomodulin; fibromodulin; PRO216; human; angiogenesis;
 KW cardiovascularisation; wound healing; cancer; atherosclerosis;
 KW cardiac hypertrophy; myocardial infarction; antiangiogenic;
 KW antitumour; tissue regeneration; pulmonary fibrosis;
 KW neurological disease; macular degeneration; diagnosis; therapy.
 XX
 OS Homo sapiens.
 XX
 XX WO9914234-A2.
 PN
 XX 25-MAR-1999.
 PD
 XX 14-SEP-1998; 98WO-US19177.
 PF
 XX 24-NOV-1997; 97US-0066772.
 PR
 XX 17-SEP-1997; 97US-0059117.
 PR
 XX 27-OCT-1997; 97US-0063329.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Fong S, Gerritsen ME, Goddard A, Gurney AL, Hillan K;

PI Williams PM, Woodwi;
 XX
 DR WPI; 1999-254381/21.
 DR N-PSDB; AAX25439.
 XX
 PT Composition containing human polypeptides with anti-angiogenic
 PT activity
 XX
 PS Example 1; Fig 6; 102pp; English.
 XX
 CC The present sequence represents human PRO216, which was identified
 CC as human osteomodulin. The sequence is predicted from cDNA clone
 CC UNQ190 or DNA33087-1158 (ATCC 209381, see AAX25439). Compositions
 CC containing PRO216, PRO230 (see AAY05764) and PRO302 (see AAY05768) in
 CC admixture with a carrier are claimed. The compositions are used to
 CC treat or prevent a wide range of cardiovascular, endothelial and
 CC angiogenic disorders (claimed), specifically cardiac hypertrophy
 CC (especially where associated with elevated levels of prostaglandin
 CC F2 alpha or induced by myocardial infarction), trauma (wounds,
 CC burns, or tissue regeneration more generally, including neurological
 CC disease), and cancer. Antagonists may be used similarly, also to
 CC treat age-related macular degeneration (or other angiogenic retinal
 CC disorders) and to prevent excessive growth of connective tissue
 CC during wound healing or in pulmonary fibrosis.
 XX
 SQ Sequence 421 AA;
 Query Match 18.4%; Score 366; DB 20; Length 421;
 Best Local Similarity 29.3%; Pred. No. 1.8e-25;
 Matches 95; Conservative 73; Mismatches 138; Indels 18; Gaps 8;
 QY 41 DDDDDDDDDDDSLFTREPSSHFFPDLFPM-CFPGCQC---YSRVVHCSDGLTSVP 96
 Db 28 DEDYDQEPDDDYQTFPFRQNVYGVPPFQHYTLGCVSECFCTPFPSSMYCDNRKLTIP 87
 QY 97 TNPFTFRLMDLNNKRIKEIKENDFKGLTSLYGLLNNKLT---TKTHPKAFLLTKLRRL 154
 Db 88 -NTPMHIQQLYLOFNEIEAVTNSFINATHLKEINLSHNKRSQKIDYGVAKLPNLLQL 146
 QY 155 YLSHNSLSEIPLNPKSLAELRIHENVKVKIQKDTFGMKNALHVLSEANPLDNGIEPG 214
 Db 147 HLEHNNLEFPFPLPKSLERLLGYNEISKLOTNAMDLVNLMTLDLCYNLHDSLLKDK 206
 QY 215 APEGV-TVPHIRIAEAKLTVPKGLPPTLLELHLDYKNKISTVELEDFKRYKELORGLGN 273
 Db 207 IFAKMEKIMQNLCSNRLESMPPLPSLSMYLSLENNSSISPEKYFDKPLKLTLMHSH 266
 QY 274 NKTTIENGSLANIPRVREIHLNENKLLK---IPSGLPKLYLIIFLHNSNIAIRGVND 330
 Db 267 NKLQDIPY-NIFNLPNIVELSVCHNKLKQAFYIPRNLEHL-----YLQNNIEKMNLTIV 319
 QY 331 FCPVTPKMKKSLYSALSIFNNPVK 354
 Db 320 MCPSIDPLHYHLTYIRVDQNKLK 343
 RESULT 42
 AAB33417
 ID AAB33417 standard; Protein; 421 AA.
 XX
 AC AAB33417;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human PRO216 protein UNQ190 SEQ ID NO:19.
 XX
 KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
 KW dermatological; antiarthritic; antiheumatic; immunosuppressive;
 KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
 KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;
 KW antischmatic; systemic lupus erythematosus; rheumatoid arthritis;
 KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;

systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 autoimmune thrombocytopenia; immune-mediated renal disease;
 demyelinating disease; hepatobiliary disease; Whipple's disease;
 inflammatory bowel disease; gluten-sensitive enteropathy;
 autoimmune disease; immune-mediated skin disease; allergic disease;
 immunological disease; transplantation associated disease;
 graft rejection; graft-versus-host-disease.

Homo sapiens.

WO200053758-A2.

14-SEP-2000.

02-MAR-2000; 2000WO-US05841.

08-MAR-1999; 99WO-US05028.
 10-MAR-1999; 99US-0123618.
 12-MAR-1999; 99US-0123957.
 23-MAR-1999; 99US-0125775.
 12-APR-1999; 99US-0128849.
 20-APR-1999; 99WO-US08615.
 28-APR-1999; 99US-0131445.
 04-MAY-1999; 99US-0132371.
 14-MAY-1999; 99US-0134287.
 22-JUN-1999; 99WO-US12252.
 23-JUN-1999; 99US-0141037.
 20-JUL-1999; 99US-0144758.
 26-JUL-1999; 99US-0145698.
 28-JUL-1999; 99US-0146222.
 01-SEP-1999; 99WO-US20111.
 08-SEP-1999; 99WO-US20594.
 13-SEP-1999; 99WO-US20944.
 15-SEP-1999; 99WO-US21090.
 15-SEP-1999; 99WO-US21547.
 05-OCT-1999; 99WO-US23089.
 29-OCT-1999; 99US-0162506.
 29-NOV-1999; 99WO-US28214.
 30-NOV-1999; 99WO-US28313.
 30-NOV-1999; 99WO-US28409.
 01-DEC-1999; 99WO-US28301.
 01-DEC-1999; 99WO-US28634.
 02-DEC-1999; 99WO-US28551.
 02-DEC-1999; 99WO-US28564.
 02-DEC-1999; 99WO-US28565.
 16-DEC-1999; 99WO-US30095.
 20-DEC-1999; 99WO-US30999.
 30-DEC-1999; 99WO-US31274.
 05-JAN-2000; 2000WO-US00219.
 06-JAN-2000; 2000WO-US00277.
 11-FEB-2000; 2000WO-US00376.
 18-FEB-2000; 2000WO-US03565.
 18-FEB-2000; 2000WO-US04341.
 22-FEB-2000; 2000WO-US04342.
 22-FEB-2000; 2000WO-US04414.

(GETH) GENENTECH INC.

Askenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
 Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

WPI: 2000-572271/53.

N-PSDB; AAC58582.

Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 arthritis, osteoarthritis, thyroiditis and diabetes mellitus -

Claim 33; Fig 8; 309pp; English.

The present invention describes sixty four human PRO proteins which can
 be used in the treatment of immune related diseases. The human PRO

CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,
 CC autoimmune or immune-mediated skin diseases, allergic diseases,
 CC immunological diseases of the lung, and transplantation associated
 CC diseases including graft rejection and graft-versus-host-disease.
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.

XX Sequence 421 AA;

Query Match 18.4%; Score 366; DB 21; Length 421;

Best Local Similarity 29.3%; Pred. No. 1.8e-25;

Matches 95; Conservative 73; Mismatches 138; Indels 18; Gaps 8;

QY 41 DDDDDDDDDNSLPTTPREPRSHFPDLFPM-CPFGQC---YSRVYHCSDLGLTVP 96

Db 28 DEDYDQEPDDDYQTGPPFRQNDYGVPPHGYTLGCVSECFCTPNFPSSMYCDNRKLKTP 87

QY 97 TNIPEDTRMLDLQNNKIKENDKGLTSLYGLIINNKL--TKIHPKAFITTKLRRL 154

Db 88 -NIPMHIOQLYQFNEIEAVTANSFINATHLKEINLSHNKIKSOKIDYGVFAKLNLQL 146

QY 155 YLHNSQLSEIPLNPKSLAELRIHENKVKIKQDKTFGMNALHVLMSANPLDNNGIEGP 214

Db 147 HLEHNLEEFPPPLPKSLERLLLYNEISKLOTNAMDGLVNLTLMDLCYNLHDSLLDK 206

QY 215 APEGV-TVFHIRTAEAKLTSVPKGLPPTLLEHLHDYINKISTVELEDFKRYKQLRLGN 273

Db 207 IFAKMEKLMQLNLCNRLESMPGLPSLMYLSLENNSSISPEKYFDKPLKHLTMRSH 266

QY 274 NKITDIENGLANIPIRVREIHLNENKLLK---IPSGLPKLYLIITFLHSNRIARVGVND 330

Db 267 NKLQDIPY-NIFNLPIVELSVCHNKLKQAFYIPRNLEHL-----YLQNNETKMLTV 319

QY 331 FCPTVPKMKSLYSALSFPNNPVK 354

Db 320 MCPSIDPLHYHLTYIRVDONK 343

RESULT 43

AAB24435

ID AAB24435 standard; Protein; 421 AA.

XX AC AAB24435;

XX AC AAB24435;

DT 07-NOV-2000 (first entry)

Human PRO216 protein sequence SEQ ID NO:227.

XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
 KW angiogenic; proliferative; cardiatic; cardiovascular; antiatherosclerotic;
 KW cytostatic; gene therapy; vaccine.

OS Homo sapiens.

XX WO200032221-A2.

PN 08-JUN-2000.

XX 30-NOV-1999; 99WO-US28313.

XX 01-DEC-1998; 98WO-US25108.

PR 16-DEC-1998; 98US-0112850.
 PR 12-JAN-1999; 99US-0115554.
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 28-APR-1999; 99US-0131445.
 PR 14-MAY-1999; 99US-0134287.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-OCT-1999; 99US-0162506.
 (GETH) GENENTECH INC.
 PI Ashkenazi AJ, Baker KP, Ferrara M, Gerber H, Hillan KJ, Goddard A;
 PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
 PI Watanabe CK, Williams PM, Wood WT;
 XX
 DR WPI; 2000-412154/35.
 DR N-PSDB; AAA77688.
 XX
 PT Nucleic acids encoding PRO polypeptides useful for preventing,
 PT diagnosing and treating disorders in mammals -
 PT angiogenic disorders in mammals -
 XX
 PS Claim 72; Fig 96; 315pp; English.
 XX
 CC The present invention describes nucleic acids encoding PRO polypeptides
 CC useful for preventing, diagnosing and treating disorders in mammals by
 CC modulating cell proliferation, angiogenesis and cardiovascularisation,
 CC and for identifying agonists and antagonists of these processes. The
 CC nucleic acids and the proteins they encode may be used in the
 CC prevention, treatment and diagnosis of diseases associated with
 CC inappropriate PRO expression such as cardiovascular, endothelial or
 CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
 CC cardiac hypertrophy). For example, the nucleic acids (NCS) and vectors
 CC containing them and the PRO polypeptide may be used to treat disorders
 CC associated with decreased PRO expression. AAA77510 to AAA77721 and
 CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in
 CC the exemplification of the present invention.
 XX
 SQ Sequence 421 AA;
 Query Match 18.4%; Score 366; DB 21; Length 421;
 Best Local Similarity 29.3%; Pred. No. 1.8e-25;
 Matches 95; Conservative 73; Mismatches 138; Indels 18; Gaps 8;
 QY 41 DDDDDDDDDSLFTTRPSHFPPDLPFM-CFPGQC---YGRVHCSDLGLTSVP 96
 DB 28 DEDYDQEPDDDYQTGFPRQVNDYGVFPFHOYTLCGVSECFCTNFPSSMYCDNRKLTIP 87
 QY 97 TNIPDFRMLDQNNKIKETKENDKGLTSLYGLILNNKL--TKTHPKAFLTTKKLRLL 154
 DB 88 -NTPMHQOQLYQFNEIEAVTANSFINATHLKEINLSHNKIKSQDKDYGVFAKLPLLQL 146
 QY 155 YLSHNSLSEIPLNPKSLAELRTHENKVKIKQDKTFGMNALHVLMSANPLDNNNGIEPG 214
 DB 147 HLEHNNLEFPPLPKSLERLLGYNFISKLQFNAMDGLVNLTMDLCTNYLHDSLEKOK 206
 QY 215 AFEGV-TVFHIRAEAKLTSVPGKLPPTLLEHLNDKNTSTVELEDFKRYKEQLRGLGN 273
 DB 207 IFARMEKLMQNLCSNRLESMPPLPSLMLYSLNNSISSIPEKYFDKLPKLHTRMSH 266
 QY 274 NKTDIDGSLANTPRVREHLENNKLLK---IPSGLPKELQIQTIFLHNSNSTARVGVND 330
 DB 267 NKLDIPY-NIFNLNIVLSVGHNKLKQAFYIPRNLEHL-----YLQNNTEKRNLTIV 319

QY 331 FCPTVPKMKKSLYSALSLFNPNVK 354
 DB 320 MCPSIDPLHYHHLTYIRVDQNKLK 343
 RESULT 44
 ID AAY88377 standard; Protein; 421 AA.
 AC AAY88377;
 XX 20-JUL-2000 (first entry)
 DE PRO216 (osteomodulin/fibromodulin homologue) protein sequence.
 KW Human; PRO216; Osteomodulin; fibromodulin; homologue; cardiatic;
 KW angiogenic; cytostatic; ophthalmic; antiproliferative activity;
 KW cardiovascular; endothelial; angiogenic disorder; cardiac hypertrophy;
 KW trauma; cancer; myocardial infarction; age-related macular degeneration.
 OS Homo sapiens.
 XX WO200015792-A2.
 PN 23-MAR-2000.
 PD 13-SEP-1999; 99WO-US20944.
 PF 14-SEP-1998; 98US-0100262.
 PR 14-SEP-1998; 98WO-US19177.
 XX (GETH) GENENTECH INC.
 PA Fong S, Gerritsen ME, Goddard A, Gurney AL, Hillan KJ;
 PI Williams PM, Wood WT;
 XX WPI: 2000-271431/23.
 DR N-PSDB; AAA13198.
 XX A composition comprising PRO230, PRO216 or PRO302 polypeptides,
 PT agonists or antagonists useful for promotion or inhibition of
 PT cardiovascularisation, angiogenesis or endothelialisation in mammals -
 PS Example 2; Fig 4; 135pp; English.
 XX
 CC This sequence represents the human PRO216 amino acid sequence. PRO216 is
 CC a human osteomodulin/fibromodulin homologue. The invention relates to a
 CC composition comprising a PRO230 (tubulointerstitial nephritis antigen
 CC homologue), PRO216 (osteomodulin/fibromodulin homologue) or PRO302
 CC (vitellogenin carboxypeptidase homologue) polypeptide, or an agonist or
 CC antagonist of these. Also included in the invention is a method for
 CC preparing the composition, agonists and antagonists of PRO230, PRO216 or
 CC PRO302, and antibodies that bind to a PRO230, PRO216 or PRO302
 CC polypeptides. The composition of the invention has cardiatic, angiogenic,
 CC cytostatic, ophthalmic, and antiproliferative activity. Analysis of the
 CC level of expression of a gene encoding a PRO230, PRO216 or PRO302
 CC polypeptide or detecting the presence/absence of the polypeptide is
 CC useful for diagnosis of cardiovascular, endothelial or angiogenic
 CC disorders in mammals. Anti-PRO230, PRO216 or PRO302 antibodies are useful
 CC in these diagnostic methods. The PRO230, PRO216 or PRO302 polypeptides
 CC (and their coding sequences), agonists and antagonists are useful for
 CC treatment of cardiovascular, endothelial or angiogenic disorders,
 CC especially cardiac hypertrophy (especially characterized by presence of
 CC an elevated level of Pgf-2alpha), trauma or cancer, myocardial infarction
 CC or age-related macular degeneration. In particular, PRO216, an agonist of
 CC PRO216, an antagonist of PRO230, PRO216 or PRO302 or an anti-PRO216
 CC antibody is useful for inhibition of endothelial cell growth in a mammal.
 CC Endothelial cell growth can be stimulated by administration of PRO230, a
 CC PRO230 agonist or antagonist or an anti-PRO230 antibody. Additionally, an
 CC anti-PRO302 antibody can inhibit angiogenesis induced by PRO302 in a
 CC mammal.

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SQ      Sequence      421 AA;
Query Match      18.4%; Score 366; DB 21; Length 421;
Best Local Similarity 29.3%; Pred. No. 1.8e-25;
Matches 95; Conservative 73; Mismatches 138; Indels 18; Gaps 8;

QY      41 DDDDDDDDDDDNSLFTTREPSSHFFDLFPM-CFPGQCQ---YSRVVHCSDGLTSTVP 96
Db      28 DEDYDQEPDDDYQTFPFRQNVYGVVPHQYTLGCYSECFCTPNFSSMYCDNRKLTIP 87

QY      97 TNIPDTRMLDLQNNKIKEKENDFKGLTSLYGLLIINNKL--TKIHPKAFLTTKKLRL 154
Db      88 -NIPMHIQQLYQFNEIEAVTANSINATHKEINLSHNKIKSQIDYGVFAKLPLNLLQ 146

QY      155 YLSHNSLSEIPLNPKSLAELRTHENKVKIKQDTEFGMNAHLVLEMSANPLDNNIEPG 214
Db      147 HLEHNNEEFPPPLPKSLERLLLYNEISKLQTNAMDGLVNLMLDLCYNLHDSLLKDK 206

QY      215 AFEGV-TVFHIRIAEAKLTSVPKGLPPTLLEHLDYNNKISTVELEDFKRYKELQRLGLN 273
Db      207 IFAKMEKLMQLNLCNSNRLESMPPLPSSLMYLSLENNISISSIPEKYFDKLPKLTLMRSH 266

QY      274 NKITDIENGSLANIPRVREIHLNENKLLK---IPSGLPPELKYLIQIIFLHNSIARVGVND 330
Db      267 NKLODIPY-NIFNLPNTIVELSVGHNKLKQAFYIPRNLHL-----YLQNNIEKMNLT 319

QY      331 FCPTVPKMKKSLYSALSFLNPNVK 354
Db      320 MCPSIDPLHYHLTYIRVDQNKLK 343

RESULT 45
AAU12322
ID      AAU12322 standard; Protein; 421 AA.
AC      AAU12322;
XX      24-OCT-2001 (first entry)
XX      Human PRO216 polypeptide sequence.
XX      Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW      breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW      cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW      adipocyte; A-peptide; factor VIIA; gene therapy.
XX      Homo sapiens.
XX      OS
XX      PN      WO200140466-A2.
XX      PD      07-JUN-2001.
XX      PF      01-DEC-2000; 2000WO-US32678.
XX      PR      01-DEC-1999; 99WO-US28301.
XX      PR      01-DEC-1999; 99WO-US28634.
XX      PR      02-DEC-1999; 99WO-US28551.
XX      PR      02-DEC-1999; 99WO-US28564.
XX      PR      02-DEC-1999; 99WO-US28565.
XX      PR      09-DEC-1999; 99US-0170262.
XX      PR      16-DEC-1999; 99WO-US30095.
XX      PR      20-DEC-1999; 99WO-US30911.
XX      PR      20-DEC-1999; 99WO-US30999.
XX      PR      30-DEC-1999; 99WO-US31243.
XX      PR      06-JAN-2000; 2000WO-US00277.
XX      PR      06-JAN-2000; 2000WO-US00376.
XX      PR      11-FEB-2000; 2000WO-US03565.
XX      PR      18-FEB-2000; 2000WO-US04341.
XX      PR      18-FEB-2000; 2000WO-US04342.
XX      PR      22-FEB-2000; 2000WO-US04414.
XX      PR      24-FEB-2000; 2000WO-US04914.
XX      PR      24-FEB-2000; 2000WO-US05004.
XX      PR      01-MAR-2000; 2000WO-US05601.

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PR      20-MAR-2000; 2000WO-US07377.
PR      21-MAR-2000; 2000WO-US07532.
PR      30-MAR-2000; 2000WO-US08439.
PR      17-MAY-2000; 2000WO-US13705.
PR      22-MAY-2000; 2000WO-US14042.
PR      30-MAY-2000; 2000WO-US14941.
PR      02-JUN-2000; 2000WO-US15284.
PR      10-NOV-2000; 2000WO-US30873.
XX      (GETH ) GENENTECH INC.
XX      Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX      Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX      Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX      WPI; 2001-408281/43.
XX      N-PSDB; AAS21394.
XX      Isolated, secretory and transmembrane PRO polypeptide used to detect
XX      other PRO polypeptides, link bioactive molecules to cells expressing
XX      PRO polypeptides, and detect the presence of mammalian tumours e.g.
XX      lung, breast, prostate, cervical
XX      Claim 12; Fig 302; 813pp; English.
XX      AAU12172-AAU12446 represent novel human secretory and transmembrane
XX      PRO polypeptides. The PRO polypeptides are useful to detect other
XX      PRO polypeptides, to link bioactive molecules to cells expressing
XX      PRO polypeptides, to modulate biological activities of cells expressing
XX      PRO polypeptides, and to detect the presence of mammalian lung, colon,
XX      breast, prostate, rectal, cervical or liver tumours by comparing PRO
XX      polypeptide expression in a cell sample to that in a control sample.
XX      Some of the 275 sequences are also useful to stimulate the release of
XX      tumour necrosis factor-alpha (TNF-alpha) from human blood, the
XX      proliferation or differentiation of chondrocytes, the proliferation or
XX      gene expression in pericyte cells, the release of proteoglycans from
XX      cartilage, the proliferation of inner ear utricular supporting cells or
XX      of T-lymphocytes, the release of a cytokine from peripheral blood
XX      monocytes (PBMCs), or the proliferation of endothelial cells. Some of
XX      the PRO polypeptides may modulate glucose or free fatty acid uptake by
XX      skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
XX      to factor VIIA. The PRO polypeptides can be used in assays to identify
XX      molecules involved in binding interactions. The polynucleotides encoding
XX      PRO polypeptides can be used to generate probes, antisense RNA/DNA,
XX      transgenic or knock out animals and can be used in gene therapy.
XX      Sequence 421 AA;

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Query Match      18.4%; Score 366; DB 22; Length 421;
Best Local Similarity 29.3%; Pred. No. 1.8e-25;
Matches 95; Conservative 73; Mismatches 138; Indels 18; Gaps 8;

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QY      41 DDDDDDDDDDDNSLFTTREPSSHFFDLFPM-CFPGQCQ---YSRVVHCSDGLTSTVP 96
Db      28 DEDYDQEPDDDYQTFPFRQNVYGVVPHQYTLGCYSECFCTPNFSSMYCDNRKLTIP 87

QY      97 TNIPDTRMLDLQNNKIKEKENDFKGLTSLYGLLIINNKL--TKIHPKAFLTTKKLRL 154
Db      88 -NIPMHIQQLYQFNEIEAVTANSINATHKEINLSHNKIKSQIDYGVFAKLPLNLLQ 146

QY      155 YLSHNSLSEIPLNPKSLAELRTHENKVKIKQDTEFGMNAHLVLEMSANPLDNNIEPG 214
Db      147 HLEHNNEEFPPPLPKSLERLLLYNEISKLQTNAMDGLVNLMLDLCYNLHDSLLKDK 206

QY      215 AFEGV-TVFHIRIAEAKLTSVPKGLPPTLLEHLDYNNKISTVELEDFKRYKELQRLGLN 273
Db      207 IFAKMEKLMQLNLCNSNRLESMPPLPSSLMYLSLENNISISSIPEKYFDKLPKLTLMRSH 266

QY      274 NKITDIENGSLANIPRVREIHLNENKLLK---IPSGLPPELKYLIQIIFLHNSIARVGVND 330
Db      267 NKLODIPY-NIFNLPNTIVELSVGHNKLKQAFYIPRNLHL-----YLQNNIEKMNLT 319

QY      331 FCPTVPKMKKSLYSALSFLNPNVK 354

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CC sclerosis, diabetes and arthritis, viral and bacterial infections,
 CC allergies and blood coagulation disorders. The present sequence is a
 CC protein of the invention.
 XX
 SQ Sequence 772 AA;

Query Match 18.4%; Score 366; DB 22; Length 772;
 Best Local Similarity 29.3%; Pred. No. 4.3e-25;
 Matches 95; Conservative 73; Mismatches 138; Indels 18; Gaps 8;

QY 41 DDDDDDDDDDDNSLFPPTREPSRSHFFDLPFM-CPFGCQC---YSRVVHCHSDGLGTSVP 96
 Db DEDYDQEPDDDDYQGTGFPFRQNVYDGVPHQYTLGCVSECFCTNPSPSSMYCDNRKRLKTP 438

QY 97 TWNPDTMDLQNNKIKKIKENDPKGLTSLYGLTLNNKL--TKIHPKAFLLTKKLRL 154
 Db 439 -NIPMHIOOLYLOFNEIEAVTANSINATLKEINLSNKKIKSOKIDYGVFAKLPNLLQL 497

QY 155 YLSHNSLSEIPLNPKSLAELRIHENKVKIKQKDTFGKGMALHVLMSANPLDNNGIEPG 214
 Db 498 HLEHNNEEFPPLPKSLERLLLYGNEISKLTQTNAMDGLVNLTMDCYNYLHDSLLKDX 557

QY 215 AFEVGV-TVEHRIARAKLTSVPKGLPPLLEHLHDYKINISVELEDFKRYKELQRLGNG 273
 Db 558 IFAPKEKLMQMLNCSNRLESMPGLPSSLMYLSLENNSSISSTPEKYPDKLPKLHTRMSH 617

QY 274 NKITDIENGSLANIPRVREIHLNKKKK---IPSGLPKLYLOIIFLHNSIARVGVND 330
 Db 618 NKLODIPY-NFNLPNIVELSVGHKLNKQAFYIPRNLEHL-----YLQNNNEIEKMLTV 670

QY 331 FQCTVPKMKKSLYSALSIFNPNVK 354
 Db 671 MCPSIDPLHYHHLTVIRVDQNK 694

RESULT 49
 AAM40226
 ID AAM40226 standard; Protein; 674 AA.
 AC AAM40226;
 XX
 XX 22-OCT-2001 (first entry)
 DE Human polypeptide SEQ ID NO 3371.
 DE Human; neutrotropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX Homo sapiens.
 OS
 XX WO200153312-A1.
 XX 26-JUL-2001.
 XX 26-DEC-2000; 2000WO-US34263.
 XX 21-JAN-2000; 2000US-0488725.
 XX 25-APR-2000; 2000US-0552317.
 XX 09-JUL-2000; 2000US-0598042.
 XX 19-JUL-2000; 2000US-0620312.
 XX 03-AUG-2000; 2000US-0853450.
 XX 14-SEP-2000; 2000US-0662191.
 XX 19-OCT-2000; 2000US-0693036.
 XX 29-NOV-2000; 2000US-0727344.
 XX (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX WPI; 2001-442253/47.
 DR N-PSDB; AA159382.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 PS Example 5; SEQ ID NO 3371; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AA42213) with neutrotropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Actin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX
 SQ Sequence 674 AA;

Query Match 18.2%; Score 363.5; DB 22; Length 674;
 Best Local Similarity 32.7%; Pred. No. 6e-25;
 Matches 92; Conservative 51; Mismatches 105; Indels 33; Gaps 7;

QY 74 CPFGCOCYSRVHCHSDGLTSPVTNPIDPDMLDLQNNKIKKIKENDPKGLTSLYGLLN 133
 Db 54 CPSCVCRDNGFIYCNDRGLTSIPADIPDDATTLYLQNNQI-----N 94

QY 134 NNKLTIKHPKAFLLTKKRLYLHNSQLSEIPLNPKSLAELRIHENKVKKQKDTFKGM 193
 Db 95 NAGI-----PODLTKYVNVQVILYENDLDEFINLPSRELHLQDNNVTRTARDSIARI 150

QY 194 NALHVLMSANPLDNNNGIEPGAF-EGVTVEFHRIAEAKLTSVPKGLPPTLLEHLHDYK 252
 Db 151 PLEKHLDDNSYSTVSIEDAFADSKQLKLLFSRNHLSIPSGUPHTLELRDDNRI 210

QY 253 STVELEDFKRYKELQRLGNNKIKTD--IENGSLANIPRVREIHLNKKIKKIPSGIPEL 310
 Db 211 STPIHAFKGLNSRLRLVDGLNLAQRIADDFSLQNLTELSELVSRNSLAAPPLNPS- 269

QY 311 KYLIQIIFLHNSIARVGVNDFCTVPKMKKSLYSALSIFNN 351
 Db 270 AHLQKLYLQDINAISHIPYN---TLAKMRE--LERLDLSNN 304

RESULT 50
 AAU12189
 ID AAU12189 standard; Protein; 674 AA.
 XX AAU12189;
 XX
 XX 24-OCT-2001 (first entry)
 XX Human PRO1483 polypeptide sequence.
 XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy.
 XX Homo sapiens.
 OS
 XX WO200140466-A2.
 XX

PD 07-JUN-2001.
XX 01-DEC-2000; 2000WO-US32678.
PF 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX

(GETH) GENENTECH INC.

XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX

DR WPI: 2001-408281/43.
N-PSDB; AAS21261.

XX Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical

PS Claim 12; Fig 36; 813pp; English.

XX AAU12172-AAU12446 represent novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing
CC PRO polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes, the release of a cytokine from peripheral blood
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIA. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.

XX Sequence 674 AA;

Query Match 18.2%; Score 363.5; DB 22; Length 674;
Best Local Similarity 32.7%; Pred. No. 6e-25;

	Matches	92; Conservative	51; Mismatches	105; Indels	33; Gaps	7;
QY 74	CPEGCQCYSRVHCSDGLT	SVPTNIPDTRMLD	QNNKIKEIKENDFKGLTSLYGLIIN	133		
DB 54	CPSVCRCDNGFIYCND	RGLTSPADIPDDATTLY	QNNQI-----N	94		
QY 134	NNKLTKIHPKAFITTK	RRRLYLSHNOISEIP	LNLPKSLAELRIHENKVKIKQKDTFKGM	193		
DB 95	NAGI----	PQDLKTKVNVQVI	YENDLDEFFINLP	SRSLRELHLQDNNVRTIARDSLARI	150	
QY 194	NALHVLEMSANPLD	NNNGIEPGAF-EGVT	VFHIRIAEAKLTSV	PKGLPPTLLEHLHDYNKI	252	
DB 151	PLEKIHLDNDSV	STVSIIEEDAFADSK	QLKLLFLSRNHLSS	IPSGLPHTLEELRDDNKI	210	
QY 253	STVELEDFKRYKEL	QRLGLGNNKITD--	LENGSLANIPRVREI	HLNKKKKIPSGLP	310	
DB 211	STIPLHAFKGLNS	RELVDGNLANQRI	ADDTFSRLQNLTEL	SLVRNSLAAPPLNLP	269	
QY 311	KYLIQIIFLHSN	SIARVGVND	FQPTVPKMKKS	LYSAISLENN	351	
DB 270	AHLQKLYLOD	NAISHIPYN---	TLAKMRE--	LERLDLSNN	304	

Search completed: January 24, 2003, 12:25:34
Job time : 42 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1799	90.3	373	4	US-09-724-864-43	Sequence 43, Appl
2	1021	51.3	368	1	US-08-303-238-3	Sequence 3, Appli
3	1021	51.3	368	4	US-08-458-834-3	Sequence 3, Appli
4	1020	51.2	368	6	5340934-2	Patent No. 5340934
5	963.5	48.4	359	1	US-08-303-238-4	Sequence 4, Appli
6	963.5	48.4	359	4	US-08-458-834-4	Sequence 4, Appli
7	949	47.6	342	1	US-08-273-919-2	Sequence 2, Appli
8	949	47.6	342	1	US-08-619-916-2	Sequence 2, Appli
9	949	47.6	342	5	PT-0595-08942-2	Sequence 2, Appli
10	947	47.5	333	1	US-08-442-063A-27	Sequence 27, Appl
11	907	45.5	353	6	5340934-4	Patent No. 5340934
12	847	42.5	307	1	US-08-442-063A-48	Sequence 48, Appl
13	776	39.0	282	1	US-08-442-063A-45	Sequence 45, Appl
14	616	30.9	236	1	US-08-442-063A-42	Sequence 42, Appl
15	493	24.7	188	1	US-08-442-063A-39	Sequence 39, Appl
16	384.5	19.3	141	1	US-08-442-063A-36	Sequence 36, Appl
17	342.5	17.2	375	1	US-08-303-238-2	Sequence 2, Appli
18	342.5	17.2	375	4	US-08-458-834-2	Sequence 2, Appli
19	336	16.9	1525	3	US-09-191-647-2	Sequence 2, Appli
20	336	16.9	1525	4	US-09-540-245A-2	Sequence 2, Appli
21	336	16.9	1525	4	US-09-540-153-2	Sequence 2, Appli
22	334.5	16.8	649	4	US-09-188-930-305	Sequence 2, Appli
23	318	16.0	376	1	US-08-303-238-1	Sequence 305, Appl
24	318	16.0	376	4	US-08-458-834-1	Sequence 1, Appli
25	316	15.9	1480	3	US-09-191-647-7	Sequence 7, Appli
26	316	15.9	1480	4	US-09-540-245A-7	Sequence 7, Appli
27	316	15.9	1480	4	US-09-540-153-7	Sequence 7, Appli

QY 301 KKIPSGLPKYLQIIFLHNSIARVGNDFCPTVPKMKKSLYSALSFLNPNPKYWEWOP 360
 Db 295 KKIPSGLPKYLQIIFLHNSIARVGNDFCPTVPKMKKSLYSALSFLNPNPKYWEIOP 354
 QY 361 ATRFCVLGRMSVQLGNFG 378
 Db 355 ATRFCVLGRMSVQLGNVG 372

RESULT 2
 US-08-303-238-3
 : Sequence 3, Application US/08303238
 : Patent No. 5654270
 : GENERAL INFORMATION:
 : APPLICANT: RUOSLAHTI, ERKKI I.
 : APPLICANT: LONGAKER, MICHAEL T.
 : APPLICANT: WHITBY, DAVID J.
 : APPLICANT: HARPER, JOHN R.
 : APPLICANT: PIERSCHBACHER, MICHAEL D.
 : APPLICANT: BORDER, WAYNE A.
 : TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
 : TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
 : NUMBER OF SEQUENCES: 8
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: CAMPBELL AND FLORES
 : STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
 : CITY: SAN DIEGO
 : STATE: CALIFORNIA
 : COUNTRY: UNITED STATES
 : ZIP: 92122
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/303,238
 : FILING DATE:
 : CLASSIFICATION: 514
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/978,931
 : FILING DATE: 17-NOV-1992
 : ATTORNEY/AGENT INFORMATION:
 : NAME: KONSKI, ANTOINETTE F.
 : REGISTRATION NUMBER: 34,202
 : REFERENCE/DOCKET NUMBER: P-LA 9453
 : TELEPHONE: 619-535-9001
 : TELEFAX: 619-535-8949
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 368 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-303-238-3

Query Match 51.3%; Score 1021; DB 1; Length 368;
 Best Local Similarity 52.4%; Pred. No. 5e-93;
 Matches 197; Conservative 64; Mismatches 95; Indels 20; Gaps 3;

QY 6 LLLFLALCAKPF-----FSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFFPTREP 61
 Db 7 LVSLALSAQLPFEQRCGFWDFTLDDGPFPMNDEEASGADTSGVLDPD-----SVTPTYS- 60

QY 62 RSHFFPDLFPMCPGCGQCYSRVHCSDGLTTSVPTNIPFTYRMLDLQNNKIKEKDNDF 121
 Db 61 -----AMCPFGCHLVRVQCSDGLKSVKPEISPTDTLLDQNNDISLRLKDDF 110

QY 122 KGLTSLYGLILNNKLTKTTHPAFLTTKKRLRYLSHNOLSEIPLNLPKSLAELRIHENK 181
 Db 111 KGLQHLVALVLYNNKLSIKHEAFSLRNVQKLYISKHNLVEIIPNPLSSVLELRHONR 170

QY 182 VKKIOKDTFKGMALHVLMSANPLDNNNGIEPGAEGVTVFHIRIAEAKLTSPVKGLPPT 241
 Db 171 IRKVPNGVPSGLRNNNCIEMGPNLENSGFEPGADGLKLVLRISAEKLTGIPKDLPET 230
 QY 242 LLELHLDYNKISTVELEDFKRYKELQRLGLGNKKTIDTENGSLANIPIVREIHLNKKLK 301
 Db 231 LNELHLDHKNKIQAIIELEDLRYSKLYRLGLGHQIRMIENGSLSPFTIRELHLDNNKLA 290
 QY 302 KIPSGLPKYLQIIFLHNSIARVGNDFCPTVPKMKKSLYSALSFLNPNPKYWEWOP 361
 Db 291 RVPISGLPDLKLVYVLSNNTKVGNDFCPMGFCVRRAYNGISLNNPVPYWEVOPA 350
 QY 362 ATRFCVLGRMSVQLGNF 377
 Db 351 ATRFCVTDRLAIQFGNY 366

RESULT 3
 US-08-458-834-3
 : Sequence 3, Application US/08458834
 : Patent No. 6277812
 : GENERAL INFORMATION:
 : APPLICANT: RUOSLAHTI, ERKKI I.
 : APPLICANT: LONGAKER, MICHAEL T.
 : APPLICANT: WHITBY, DAVID J.
 : APPLICANT: HARPER, JOHN R.
 : APPLICANT: PIERSCHBACHER, MICHAEL D.
 : APPLICANT: BORDER, WAYNE A.
 : TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
 : TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
 : NUMBER OF SEQUENCES: 8
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: CAMPBELL AND FLORES
 : STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
 : CITY: SAN DIEGO
 : STATE: CALIFORNIA
 : COUNTRY: UNITED STATES
 : ZIP: 92122
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/458,834
 : FILING DATE:
 : CLASSIFICATION: 514
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/978,931
 : FILING DATE: 17-NOV-1992
 : ATTORNEY/AGENT INFORMATION:
 : NAME: KONSKI, ANTOINETTE F.
 : REGISTRATION NUMBER: 34,202
 : REFERENCE/DOCKET NUMBER: P-LA 9453
 : TELEPHONE: 619-535-9001
 : TELEFAX: 619-535-8949
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 368 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-458-834-3

Query Match 51.3%; Score 1021; DB 4; Length 368;
 Best Local Similarity 52.4%; Pred. No. 5e-93;
 Matches 197; Conservative 64; Mismatches 95; Indels 20; Gaps 3;

QY 6 LLLFLALCAKPF-----FSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFFPTREP 61
 Db 7 LVSLALSAQLPFEQRCGFWDFTLDDGPFPMNDEEASGADTSGVLDPD-----SVTPTYS- 60

QY 62 RSHFPFDLPMPGCGOCYSRVVHCSDLGLTSVPTNIPEDTRMLDLQNNKIKEKENDF 121
 Db 61 -----AMCPGCHLRVQCSDLGLKSVKESPDITLDDQNNDISLKRKDDF 110
 QY 122 KGLTSLYGLILNNKLTIKHPKAFITTKKRLRLYLSHNQLSEIPLNLPKSLAEIRIHENK 181
 Db 111 KGLQHLALVNLNNKISKIHEKAFSPLRNVQKLYISKHNLVEIPNLPSSLSVELRIHNR 170
 QY 182 VKKIQDFTKGMNALHVLMSANPLDNGIEPGAFEGVTVPHIRIAEAKLTSVPKGLPPT 241
 Db 171 IRKVPNGVFSGLRNMNCIEMGNPLENSGFEFGADGLKLYLRISAEAKLTGIPKDLPET 230
 QY 242 LLELHLDYKISTVELEDFKRYKEQLRGLGNKKTITDENGSLANIPRVREIHLNENK 301
 Db 231 LNELHLDHKNQIAIELELLRYSKLYRLGLGHQIRMIENGSLFPLTRELHLDNNKLA 290
 QY 302 KIPSGLPKLYLOIIFLHNSNARVGVNDFCPTVPMKKSLSAISLNNPVKYWQPA 361
 Db 291 RVPSPGLPKLLQVYLHNSNITKVGNDFCPMGFGVKRAYNGISLNNPVKYWQPA 350
 QY 362 TFCVLSRMSVOLGNF 377
 Db 351 TPCVTDLRAIQFGNY 366

RESULT 4

5340934-2

; Patent No. 5340934

; ROBEY, PAMELA G.

; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS

; NUMBER OF SEQUENCES: 13

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/432,044

; FILING DATE: 03-NOV-1989

; SEQ ID NO: 2

; LENGTH: 368

5340934-2

Query Match 51.2%; Score 1020; DB 6; Length 368;
 Best Local Similarity 52.1%; Pred. No. 6.3e-93;
 Matches 196; Conservative 66; Mismatches 94; Indels 20; Gaps 3;
 QY 6 LILFLALCSAKPF-----FSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPTR 61
 Db 7 LVSLALSQLAPFEQRGWDFTLDDGPFMMNDEASGADTSGVLDPD-----SVTPYS- 60

QY 62 RSHFPFDLPMPGCGOCYSRVVHCSDLGLTSVPTNIPEDTRMLDLQNNKIKEKENDF 121
 Db 61 -----AMCPGCHLRVQCSDLGLKSVKESPDITLDDQNNDISLKRKDDF 110
 QY 122 KGLTSLYGLILNNKLTIKHPKAFITTKKRLRLYLSHNQLSEIPLNLPKSLAEIRIHENK 181
 Db 111 KGLQHLALVNLNNKISKIHEKAFSPLRNVQKLYISKHNLVEIPNLPSSLSVELRIHNR 170
 QY 182 VKKIQDFTKGMNALHVLMSANPLDNGIEPGAFEGVTVPHIRIAEAKLTSVPKGLPPT 241
 Db 171 IRKVPNGVFSGLRNMNCIEMGNPLENSGFEFGADGLKLYLRISAEAKLTGIPKDLPET 230
 QY 242 LLELHLDYKISTVELEDFKRYKEQLRGLGNKKTITDENGSLANIPRVREIHLNENK 301
 Db 231 LNELHLDHKNQIAIELELLRYSKLYRLGLGHQIRMIENGSLFPLTRELHLDNNKLA 290
 QY 302 KIPSGLPKLYLOIIFLHNSNARVGVNDFCPTVPMKKSLSAISLNNPVKYWQPA 361
 Db 291 RVPSPGLPKLLQVYLHNSNITKVGNDFCPMGFGVKRAYNGISLNNPVKYWQPA 350
 QY 362 TFCVLSRMSVOLGNF 377
 Db 351 TPCVTDLRAIQFGNY 366

RESULT 5

US-08-303-238-4

; Sequence 4, Application US/08303238

; Patent No. 5654270

; GENERAL INFORMATION:

; APPLICANT: RUOSLAHTI, ERKKI I.

; APPLICANT: LONGAKER, MICHAEL T.

; APPLICANT: WHITBY, DAVID J.

; APPLICANT: HARPER, JOHN R.

; APPLICANT: PIERSCHBACHER, MICHAEL D.

; APPLICANT: BORDER, WAYNE A.

; TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CAMPBELL AND FLORES

; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700

; CITY: SAN DIEGO

; STATE: CALIFORNIA

; COUNTRY: UNITED STATES

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/303,238

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/978,931

; FILING DATE: 17-NOV-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: KONSKI, ANTOINETTE F.

; REGISTRATION NUMBER: 34,202

; REFERENCE/DOCKET NUMBER: P-LA 9453

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-535-9001

; TELEFAX: 619-535-8949

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 359 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-303-238-4

Query Match 48.4%; Score 963.5; DB 1; Length 359;
 Best Local Similarity 50.4%; Pred. No. 2.4e-87;
 Matches 191; Conservative 65; Mismatches 100; Indels 23; Gaps 4;
 QY 1 MKEYVILLFLALCS-AKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPTR 59
 Db 1 MKATITILLIAQVSWAGPF---QQRGLEDFMLEDEASGIGPEVPPDRD----- 45
 QY 60 EPRSHEFPFDLPMPGCGOCYSRVVHCSDLGLTSVPTNIPEDTRMLDLQNNKIKEKEN 119
 Db 46 -----FEPGLGVPFCFQCHQVQCSDLGLDKVVKDLPPDTTLLDQNNKITEIKDG 99
 QY 120 DFGLTSLYGLILNNKLTIKHPKAFITTKKRLRLYLSHNQLSEIPLNLPKSLAEIRIHE 179
 Db 100 DFNKLNHALILVNNKISKVSPGATPLVKLERLYSKNQLKELPEKPKTKLOELRAHE 159
 QY 180 NKYKTKQDFTKGMNALHVLMSANPLDNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGL 238
 Db 160 NEITKRVKTVFNGLNQIMIVIELGTNPLKSSGIENGAFQGMKLSYRIADTNITSIPOGL 219
 QY 239 PPTLLELHLDYKISTVELEDFKRYKEQLRGLGNKKTITDENGSLANIPRVREIHLNEN 298
 Db 220 PPSLTELHLDGNKISRVDASLAKGLNLANLAKGLSFSNLSAVDNGSLANTPHLRELHLDNN 279
 QY 299 KKKKIPSGLPKLYLOIIFLHNSNARVGVNDFCPTVPMKKSLSAISLNNPVKYWEM 358

Db	160	NEITKRVKVTNGLNOMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTNTITSPOQL	219
QY	239	PPTLLELHDYDKISITVELEDFRRYKELQPLGLGNKKITDIENGSLANTPRVREIHLNN	298
Db	220	PPSLTELHLDGKISRVDAAASLKGKLNLAKLGLSFNISAVDNGSLANTPHRLHLDNN	279
QY	299	KLKIPSGELPKYLIIFLHNSIARVGVNDFCPTVRMKKSLYSALISLNNPVKYYEM	358
Db	280	KLTRVPGGLAEHKYIQVYLHNNNISVVGSDFCPPGHNTKASYSGVSLFSNPVQYWEI	339
QY	359	QPATFRCVLSRMSVQLGNF	377
Db	340	OPSTFRCCVYVRSIOLGNY	358

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Db      280 KLTRVPGGLAEHRYIOVVYLNHNINISVGSSDFCPPGHNTKKASYSGVSLFSNPQYWEI 339
          ||::|||::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy      359 QPATERCVLSRMSVOLGNF 377
          ||::|||::||::||::||::||::||::||::||::||::||::||::||::||
Db      340 QPSTFCRVVRSAILGNY 358
          ||::|||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 7
US-08-272-919-2
; Sequence 2, Application US/08272919
; Patent No. 5567807
; GENERAL INFORMATION:
; APPLICANT: Craig, William S.
; APPLICANT: Harper, John R.
; APPLICANT: Hernandez, Sam D.
; APPLICANT: Kostel, Paul J.
; APPLICANT: Parker, Jonathan R.
; APPLICANT: Vedvick, Thomas S.
; TITLE OF INVENTION: Processes for the Purification of Human
; TITLE OF INVENTION: Recombinant Decorin and the Detection of Guanidinium Ions
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,919
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PS-08-272-919-2

```

```

; LENGTH: 342 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-272-919-2

Query Match 47.6%; Score 949; DB 1; Length 342;
Best Local Similarity 53.9%; Pred. No. 6.1e-86;
Matches 178; Conservative 63; Mismatches 87; Indels 2; Gaps

Qy 49 DEDNSLFTPREKSHFFPDLPMPGFCQCYSRVVHCSDLGLGTSVPTWIPEDTRMLDL 108
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 14 EDEASGIGP-EVPPDRDFEFSGLGVCFRCQCHLRVQCSDGLGLDKVPKDLPPDTLLDL 72

Qy 109 QNNKIKEIKENDFKGLTSLYGLLIINNKKLTIIIPKAPLTTKKLRRLYLSHNQLSEIPLN 168
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 73 QNNKITIKDGFKNKLNALIIINNKKISKVSPGFTPLVKRLRYLSNKKLPEKPM 132

```

QY 169 PKSLAELRIHENKVKIKQKDTFGKGMALHVLMSANPLDNNNGIEPGAFEGV-TVFHRIA 227
Db 133 PKTLOELRAHENEITKVRKVTNGLNQMIVIELCTNPLKSSGLNGAFQGMKLSYRIA 192
QY 228 EAKITSVKGLPPTLELHLDYNKISTVELEDFKRYKELQRLGKGNKKTIDINGSLANI 287
Db 193 DTNITSIPQGLPPTLELHLDYNKISTVELEDFKRYKELQRLGKGNKKTIDINGSLANI 252
QY 288 PRVREIHLNENKIKIPSGLPKYLQIIFLHNSIARVGVNDFCPTVPKMKKLSYSAIS 347
Db 253 PHLRELHLDNNKLRVPGGLAEHKYIQVYVYLNHNNSISVVGSSDFCPCPGHNTKASYSVGS 312
RESULT 8
US-08-619-916-2
; Sequence 2, Application US/08619916
; Patent No. 5763276
; GENERAL INFORMATION:
; APPLICANT: Craig, William S.
; APPLICANT: Harper, John R.
; APPLICANT: Hernandez, Sam D.
; APPLICANT: Kostel, Paul J.
; APPLICANT: Parker, Jonathan R.
; APPLICANT: Vedvick, Thomas S.
; TITLE OF INVENTION: Processes for the Purification of Human
; TITLE OF INVENTION: Recombinant Decorin and the Detection of Guanidinium Ions
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/619,916
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,919
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-619-916-2

Query Match 47.6%; Score 949; DB 1; Length 342;
Best Local Similarity 53.9%; Pred. No. 6.1e-86;
Matches 178; Conservative 63; Mismatches 87; Indels 2; Gaps 2;

QY 49 DDEDSLFPTRPRSHFFPDLPMPGFCQCYSRVHCSDGLGTSVPTNIPDTRMLDL 108
Db 14 EDEASGIGP-EVDDRDPEPSLGPVCPFRCHLRVQCSDLGLDKVDPKDLPPDPTLLDL 72

QY 109 QNNKIKEIKENDFKGLTSLYGLILNANNKLTIKHPKAFLTTKLRLYLSHNSQLSEIPLNL 168
Db 73 QNNKITEIKDGFKNLKNLHALLVNNKISKVSPGAFPLVLRERLYLSKNQLKELPEKM 132
QY 169 PKSLAELRIHENKVKIKQKDTFGKGMALHVLMSANPLDNNNGIEPGAFEGV-TVFHRIA 227
Db 133 PKTLOELRAHENEITKVRKVTNGLNQMIVIELCTNPLKSSGLNGAFQGMKLSYRIA 192
QY 228 EAKITSVKGLPPTLELHLDYNKISTVELEDFKRYKELQRLGKGNKKTIDINGSLANI 287
Db 193 DTNITSIPQGLPPTLELHLDYNKISTVELEDFKRYKELQRLGKGNKKTIDINGSLANI 252
QY 288 PRVREIHLNENKIKIPSGLPKYLQIIFLHNSIARVGVNDFCPTVPKMKKLSYSAIS 347
Db 253 PHLRELHLDNNKLRVPGGLAEHKYIQVYVYLNHNNSISVVGSSDFCPCPGHNTKASYSVGS 312
QY 348 LFNNPVKYWEMQPAFCRVCILSRMSVOLGNF 377
Db 313 LFSNPVQYWEIQPSTFCRCVYVRSALQGNV 342
RESULT 9
PCT-US95-08542-2
; Sequence 2, Application PC/TUS9508542
; GENERAL INFORMATION:
; APPLICANT: La Jolla Cancer Research Foundation
; TITLE OF INVENTION: Processes for the Purification of
; TITLE OF INVENTION: Human
; TITLE OF INVENTION: Recombinant Decorin and the Detection of Guanidinium
; TITLE OF INVENTION: Ions
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08542
; FILING DATE: 07-JUL-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Susan M.
; REGISTRATION NUMBER: 36,405
; REFERENCE/DOCKET NUMBER: FP-LA 1751
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-08542-2

Query Match 47.6%; Score 949; DB 5; Length 342;
Best Local Similarity 53.9%; Pred. No. 6.1e-86;
Matches 178; Conservative 63; Mismatches 87; Indels 2; Gaps 2;

QY 49 DDEDSLFPTRPRSHFFPDLPMPGFCQCYSRVHCSDGLGTSVPTNIPDTRMLDL 108
Db 14 EDEASGIGP-EVDDRDPEPSLGPVCPFRCHLRVQCSDLGLDKVDPKDLPPDPTLLDL 72
QY 109 QNNKIKEIKENDFKGLTSLYGLILNANNKLTIKHPKAFLTTKLRLYLSHNSQLSEIPLNL 168
Db 73 QNNKITEIKDGFKNLKNLHALLVNNKISKVSPGAFPLVLRERLYLSKNQLKELPEKM 132

50 DEDNSLFPTREPRSHFFPFDLFPMCPFGCCOCYSRVVHCSDGLTSTVPTNIPFDTMLDLQ 109
 || : | | | : || : || || || || || || || || : || : || ||
 3 DEASGIGP-EVPDDRDREPSLGPVCFRCQCHLRVVQCSDGLGDKVPKDLPPDPTLLDLQ 61

RESULT 12
US-08-442-063A-48
; Sequence 48, Application US/08442063A
; Patent No. 5705609
; GENERAL INFORMATION:

Patent No. 5654270
GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
APPLICANT: WHITBY, DAVID J.
APPLICANT: HARPER, JOHN R.
APPLICANT: PIERSCHBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,238
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-LA 9453
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-303-238-1

Query Match 16.0%; Score 318; DB 1; Length 376;
Best Local Similarity 26.1%; Pred. No. 2.5e-23;
Matches 86; Conservative 65; Mismatches 131; Indels 48; Gaps 9;

QY 63 SHFFPFDLFP-----CPFGCQC---YSRVVHCSDLG 91
DB 37 TYIDPYDPIYETEPYGVDEGPATYGSPPDRCPDPCDPPNFLTAMYCDNRN 96
QY 92 LTSVPTNIPDTRMLDQNNKIKEIKENDFKGLTSLYGLILNNKLT--KIHPKAFLTTK 149
DB 97 LKYLPP-VPSRMKYVYFQNNQITSIQGVDFNATGLLWIALHGNQITSDKVGKRVFSKLR 155
QY 150 KLRRLYLSHNSLSEIPLNPKSLAELRIHENKVKIKQDFTKGMNALHVLEMSANPLDNN 209
DB 156 HLRLYLHNNLTNMPGPLPSRLRELHLDHNOISRVPNNALEGLNLTALYLQHDEIQEV 215
QY 210 GIEPAGFEGV-TVFHIRIAEAKLTSPKGLPPTLLELHLDYKISTVELEDFKRYKELQR 268
DB 216 G---SSMRGLSLLILDLNSYHLNRKVPDGLPSALEQLYMEHNNVYTPDSYFRGAPKLLY 272
QY 269 LGLGNKKTIDENGLA-----NIPRVREIHLNNKIKKIPSGLPKYLQIIFLHNSIA 324
DB 273 VRLSHNSLT---NNGLASNTFSSSLLLELDLSYNOLQKIP---PVNTNLENLYLQGNRIN 326
QY 325 RVGNDECPYTPKMKKSLYSALISLFPNPK 354
DB 327 EFSISSECTVVDVNFVFSKLVRLDGNIEK 356

RESULT 24
US-08-458-834-1
Sequence 1, Application US/08458834
Patent No. 6277812
GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
APPLICANT: WHITBY, DAVID J.
APPLICANT: HARPER, JOHN R.
APPLICANT: PIERSCHBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,834
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-LA 9453
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-834-1

Query Match 16.0%; Score 318; DB 4; Length 376;
Best Local Similarity 26.1%; Pred. No. 2.5e-23;
Matches 86; Conservative 65; Mismatches 131; Indels 48; Gaps 9;

QY 63 SHFFPFDLFP-----CPFGCQC---YSRVVHCSDLG 91
DB 37 TYIDPYDPIYETEPYGVDEGPATYGSPPDRCPDPCDPPNFLTAMYCDNRN 96
QY 92 LTSVPTNIPDTRMLDQNNKIKEIKENDFKGLTSLYGLILNNKLT--KIHPKAFLTTK 149
DB 97 LKYLPP-VPSRMKYVYFQNNQITSIQGVDFNATGLLWIALHGNQITSDKVGKRVFSKLR 155
QY 150 KLRRLYLSHNSLSEIPLNPKSLAELRIHENKVKIKQDFTKGMNALHVLEMSANPLDNN 209
DB 156 HLRLYLHNNLTNMPGPLPSRLRELHLDHNOISRVPNNALEGLNLTALYLQHDEIQEV 215
QY 210 GIEPAGFEGV-TVFHIRIAEAKLTSPKGLPPTLLELHLDYKISTVELEDFKRYKELQR 268
DB 216 G---SSMRGLSLLILDLNSYHLNRKVPDGLPSALEQLYMEHNNVYTPDSYFRGAPKLLY 272
QY 269 LGLGNKKTIDENGLA-----NIPRVREIHLNNKIKKIPSGLPKYLQIIFLHNSIA 324
DB 273 VRLSHNSLT---NNGLASNTFSSSLLLELDLSYNOLQKIP---PVNTNLENLYLQGNRIN 326

[illegible]

```

Query Match      15.9%; Score 316; DB 4; Length 1480;
Best Local Similarity 25.1%; Pred. No. 3e-22;
Matches 98; Conservative 66; Mismatches 123; Indels 104; Gaps 9;

QY 74 CPFGCQCYSRVHCSDLGLTSVPTNIPDFT-----RMLDLQ 109
Db 73 CPVCSCTGLNVDCSHRGTSVPRKISADVERLELQGNLTIVYETDFQRLTKRLMLQLT 132
QY 110 NKKIKEIKENDFKGLTSYGLLNNKLTTHPKAFITTKLRLRLYLSHNLSLSEIPLNLP 169
Db 133 DNOIHTIERNFQDLVSLERLDSINNVITTVGRVFKGAQSLRSQLDNNQITCLDEHAF 192
QY 170 KSLAELRI---HENKVKIKQDKTFKGMNALHVLMSANPL----- 206
Db 193 KGLVEILEITLNNNLTSLPHNIFGGLRRLALRLSDNPFACDCHLSWLSRFLRSATRLA 252
QY 207 -----DNNGLEPGA-----FEGVTVFHRI 226
Db 253 PYTRCQSPQKQONVADLHDOEFKCSGLTEHAPMECGAENSCPHPCRCADGI----VDC 308
QY 227 AEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNKNTDIENGSLAN 286
Db 309 REKSLTSVPVTLDDTDVRLQNFITELPPKSFSSFRRLRIDLNNNISRIADHLSG 368
QY 287 IPRVREIHLENNKLIKIPSGI-PELKYLIQIIFLHNSIARVGVNDPCTVPMKKSLEY-- 343
Db 369 LKQLTTLVLYGNKIKDLPQGVFKGLSLRLLLNANEISCIKDAF-----RDLHSL 420
QY 344 SALSLENNPVKWEQMPATFRCVLSRMSVOL 374
Db 421 SLLSLYDNNIQ--SLANGTFDAMKSMKTIVHL 449

RESULT 28
PCT-US91-09055-2
Sequence 2, Application PC/TUS9109055
GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan Marc and Artavanis-Tsakonas, Spyridon
TITLE OF INVENTION: Purified SLIT protein and Sequence Elements Thereof
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yale University
ADDRESS: Office of Cooperative Research
STREET: 246 Church Street
CITY: Suite 401
STATE: New Haven
COUNTRY: Connecticut
ZIP: 06510
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/09055
FILING DATE: 19911127
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/624,135
FILING DATE: 7-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barth, Richard J.
REGISTRATION NUMBER: 28,180
REFERENCE/DOCKET NUMBER: 900964/RSB
TELEPHONE: (212) 972-1400
TELEFAX: (212) 370-1622
TELEX: 236268
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1480 amino acids
TYPE: AMINO ACIDS

```

```

; TOPOLOGY: Linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: signal sequence
; LOCATION: 1 to 36
; IDENTIFICATION METHOD: similarity to other signal
; OTHER INFORMATION: Directs Export
; NAME/KEY: Four Flank-LRR-Flank domains
; LOCATION: 37 to 910
; IDENTIFICATION METHOD: Array of Flank-LRR-Flank
; OTHER INFORMATION: mediates adhesive events
; NAME/KEY: Tandem EGF-like repeats
; LOCATION: 911 to 1150
; IDENTIFICATION METHOD: similarity to tandem EGF-like
; OTHER INFORMATION: protein-protein interactions
; NAME/KEY: 7th EGF-like repeat
; LOCATION: 1353 to 1393
; IDENTIFICATION METHOD: similarity to epidermal growth
; OTHER INFORMATION: Involvement in receptor-ligand
; NAME/KEY: Alternative splice segment
; LOCATION: 1394 to 1404
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: developmentally regulated
; NAME/KEY: COOH-terminal region
; LOCATION: 1405 to 1480
; IDENTIFICATION METHOD: experimental
; PCT-US91-09055-2

Query Match      15.9%; Score 316; DB 5; Length 1480;
Best Local Similarity 25.1%; Pred. No. 3e-22;
Matches 98; Conservative 66; Mismatches 123; Indels 104; Gaps 9;

QY 74 CPFGCQCYSRVHCSDLGLTSVPTNIPDFT-----RMLDLQ 109
Db 73 CPVCSCTGLNVDCSHRGTSVPRKISADVERLELQGNLTIVYETDFQRLTKRLMLQLT 132
QY 110 NKKIKEIKENDFKGLTSYGLLNNKLTTHPKAFITTKLRLRLYLSHNLSLSEIPLNLP 169
Db 133 DNOIHTIERNFQDLVSLERLDSINNVITTVGRVFKGAQSLRSQLDNNQITCLDEHAF 192
QY 170 KSLAELRI---HENKVKIKQDKTFKGMNALHVLMSANPL----- 206
Db 193 KGLVEILEITLNNNLTSLPHNIFGGLRRLALRLSDNPFACDCHLSWLSRFLRSATRLA 252
QY 207 -----DNNGLEPGA-----FEGVTVFHRI 226
Db 253 PYTRCQSPQKQONVADLHDOEFKCSGLTEHAPMECGAENSCPHPCRCADGI----VDC 308
QY 227 AEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNKNTDIENGSLAN 286
Db 309 REKSLTSVPVTLDDTDVRLQNFITELPPKSFSSFRRLRIDLNNNISRIADHLSG 368
QY 287 IPRVREIHLENNKLIKIPSGI-PELKYLIQIIFLHNSIARVGVNDPCTVPMKKSLEY-- 343
Db 369 LKQLTTLVLYGNKIKDLPQGVFKGLSLRLLLNANEISCIKDAF-----RDLHSL 420
QY 344 SALSLENNPVKWEQMPATFRCVLSRMSVOL 374
Db 421 SLLSLYDNNIQ--SLANGTFDAMKSMKTIVHL 449

RESULT 29
US-09-182-024A-5
Sequence 5, Application US/09182024A
Patent No. 6342370
GENERAL INFORMATION:
APPLICANT: Connolly, Timothy
APPLICANT: Rajput, Bhanu
TITLE OF INVENTION: Human Slit Polypeptide and Polynucleotides Encoding
TITLE OF INVENTION: Same
FILE REFERENCE: 640100-271
CURRENT APPLICATION NUMBER: US/09/182,024A
CURRENT FILING DATE: 1998-10-29

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Query Match	15.5%;	Score 309;	DB 4;	Length 1523;
Best Local Similarity	24.9%;	Pred. No. 1.5e-21;		
Matches 98;	Conservative	58;	Mismatches 114;	Indels 124;
				Gaps 9;

US-08-986-485-5

Query Match 14.9%; Score 296; DB 3; Length 1091;
Best Local Similarity 30.1%; Pred. No. 1.8e-20;
Matches 94; Conservative 64; Mismatches 124; Indels 30; Gaps 12;

QY 74 CPGGQCVSVVHCSDLGLTSYPTNPEDTRMLDQNNKIKKIEKENDFKGLTSYGLIIN 133
Db 43 CAACTACAGNSUDCSGRGLATLPRLPSWTRSLNLSNRLSEIDSAAPEDLTNQEVYIN 102
QY 134 NKKLKIIPKAFITTKKRLRYLSHNLSEI---PLNLPKSLAEURLIHENKVKIKQDTF 190
Db 103 SNEITAI-PSUGTAGISGVVSLFQHNKILSDVGSQKLSYLSLEVLDSLSSNNITIRSCF 161
QY 191 KGMNALHVLMSANPLDNGI---EPGAFEGV--TVFHIRIAEAKLTSVP--KGLP-PTLL 243
Db 162 P--NGLRIEIN--LASNRISLESAGAFDGLSRLTLRLSKNRTIQLPVKAFKLPRLT 216
QY 244 ELHLYNKISTVELEDFRYKELQRLGNNKITDIENGSLANIPRVREIHLNENKIKKI 303
Db 217 QDLNRRNRIEGLTFOGLDSLEVLRLQNNISRLTDGAFWGLSKMHVHLEYNLSLEV 276
QY 304 PSG-LPELKYLIQIIFLHNSIARVCVN--DFCPTVPKMKKSLYSALISLNNPVKYWQ 360
Db 277 NSGSLYGLTALHQLHLSNNSISRIQDGNWFC-----QKLHELILSFNNLTIRLDESL 329
QY 361 ATFCVLSRMSV 372
Db 330 AE---LSSLSI 337

RESULT 32

US-08-190-802A-50
; Sequence 50, Application US/08190802A
; Patent No. 5519003

; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER:
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960

; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:

; INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
; INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
US-08-190-802A-50

Query Match 13.7%; Score 272; DB 1; Length 603;
Best Local Similarity 28.2%; Pred. No. 1.8e-18;
Matches 90; Conservative 57; Mismatches 108; Indels 64; Gaps 12;
QY 102 DTRMLDQNNKIKKIEKENDFKGLTSYGLIINNNKUTKHPKRAFLTKKRLRYLSHNL 161
Db 219 ELRELDLSNRALSKVANVHLPRLQKLYLDRLNLITAVAPGAFGLMKALRWLDLSHNRV 278
QY 162 SET-----PKS-----LAEIRHENKVKIKQDTFKGMN 194
Db 279 AGLMEDTFFCLLGLHVLRIAHNAIASLRPTFKDLHLEELQLGHNRIQLGERTFEGLG 338
QY 195 ALHVLMSANPLDNGIEPGAFEGVTVFHIRIAEAK---LTSVP-----KGLPPTLLEHL 247
Db 339 QLEVLTLNDNQITE--VRVGAESG--LFNVAVMNLGNCRLSLPERVFOGL-DKLHSLHL 393
QY 248 DYNNKISTVELEDFRYKELQRLGNNKITDIENGSLANIPRVREIHLNENKIKKI 304
Db 394 EESCLGHVRLHFTAGLSGRLRLFRDNRNLSISIEEQSLAGLSLELDLTNRLTHLPROL 453
QY 305 -SGLPELKYLIQIIFLHNSIARVCVNDFCPT-----VPMKKKSLYSA----- 345
Db 454 FQGLGHLEYL---LLSYNQLITLSAEVLGQLQRAFWDISHNHLETLARGLFSSLSLGRVRY 510
QY 346 ISLFNNPVKYWQPATFR 364
Db 511 LSLRNNSLQTFSPQGLER 529

RESULT 33

US-08-477-346-50
; Sequence 50, Application US/08477346
; Patent No. 6262023

; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER:
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/487,072
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 amino acids
; TYPE: amino acid

TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
US-08-477-346-50

Query Match 13.7%; Score 272; DB 4; Length 603;
Best Local Similarity 28.2%; Pred. No. 1.8e-18;
Matches 90; Conservative 57; Mismatches 108; Indels 64; Gaps 12;

QY 102 DTRMLDQNNKIKENDEKGLTSLYGLILNNKLTTHPKAPLTTHKLRRLYLHNQ 161
DB 219 ELRELDLSRNALRSVKANFVHLPRQLKLYLDRNLITAVAPGAFGLMKALRWLDLSHNRV 278
QY 162 SEI-----PLNL-----PKS-----LAELRIHENKVKTKQKDTFKGMN 194
DB 279 AGLMEDTFPGLGLHVLRAHNAIASLRPTFKDLHFLLEQLGHNRIQLGERTFEGLG 338
QY 195 ALHVLEMSANPLDNGIPEGAFEGVTVFHIRIAEAK-----LTSVP-----KGLPPTLLEHL 247
DB 339 QLEVLTLNDNQITE--VRVGAFSG--LFNVAVMNLSCNLSRSLPERVFOGL-DKLHSLHL 393
QY 248 DYNKISTVELEDPKRYKELORGLGNKKTIDENGSLANIPRVREIHLNKKLKKIP--- 304
DB 394 EHSCLGHVRLHTFAGLSGLRLFLRDNSSISIEEQSLAGLSELELDLTTNRLTHLPRL 453
QY 305 -SGLPELKYLIQIFLHNSIARVGVNDFCPT-----VPMKKKSLISA----- 345
DB 454 FQGLGHLEYL---LLSYNQLTLSAEVLGPLQRAFWDISHNHLETLAEGFLSSIGRVRY 510
QY 346 ISLFNPNPKYWMQPATFR 364
DB 511 LSLRNSLQTFSPQGLER 529

RESULT 34

US-08-473-089-50

Sequence 50, Application US/08473089

Patent No. 6342368

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/473,089

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2550-0025.22

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 603 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
US-08-473-089-50

Query Match 13.7%; Score 272; DB 4; Length 603;
Best Local Similarity 28.2%; Pred. No. 1.8e-18;
Matches 90; Conservative 57; Mismatches 108; Indels 64; Gaps 12;

QY 102 DTRMLDQNNKIKENDEKGLTSLYGLILNNKLTTHPKAPLTTHKLRRLYLHNQ 161
DB 219 ELRELDLSRNALRSVKANFVHLPRQLKLYLDRNLITAVAPGAFGLMKALRWLDLSHNRV 278
QY 162 SEI-----PLNL-----PKS-----LAELRIHENKVKTKQKDTFKGMN 194
DB 279 AGLMEDTFPGLGLHVLRAHNAIASLRPTFKDLHFLLEQLGHNRIQLGERTFEGLG 338
QY 195 ALHVLEMSANPLDNGIPEGAFEGVTVFHIRIAEAK-----LTSVP-----KGLPPTLLEHL 247
DB 339 QLEVLTLNDNQITE--VRVGAFSG--LFNVAVMNLSCNLSRSLPERVFOGL-DKLHSLHL 393
QY 248 DYNKISTVELEDPKRYKELORGLGNKKTIDENGSLANIPRVREIHLNKKLKKIP--- 304
DB 394 EHSCLGHVRLHTFAGLSGLRLFLRDNSSISIEEQSLAGLSELELDLTTNRLTHLPRL 453
QY 305 -SGLPELKYLIQIFLHNSIARVGVNDFCPT-----VPMKKKSLISA----- 345
DB 454 FQGLGHLEYL---LLSYNQLTLSAEVLGPLQRAFWDISHNHLETLAEGFLSSIGRVRY 510
QY 346 ISLFNPNPKYWMQPATFR 364
DB 511 LSLRNSLQTFSPQGLER 529

RESULT 35

US-08-487-072A-50

Sequence 50, Application US/08487072A

Patent No. 6423684

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,072A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2550-0025.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763


```

Best Local Similarity 23.2%, Pred. No. 7.6e-17;
Matches 83; Conservative 69; Mismatches 120; Indels 85; Gaps 10;

QY 78 CQCYRVHCSDLGTSVPTPTEDTRMLDQNNKIKEIKENDFKGLTSLYGLLNKKL 137
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 52 CTCAGSDLDGCGGLAALPGDLPSWTRSLNLSYNKLAIEDIPAGFEDLPNIQYVLNNHEL 111
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 138 TKI-----HPKAFLT----- 147
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 112 TAVASLGAGSSQVWALFQQOONKSLDGSQKLYSLLEVLDLNLTITEVRNYFPHPGP 171
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 148 -----TKKRLRYLSHNOLSEIP----- 182
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 172 IKELNLAGNRICTELGAFDGLSRSLTLRLSKNRITQLPVRAFKLPR-LTQLDLNRRI 230
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 183 KTKQDFTFGMNALHVLEMSANPLDNNIEPGAGEGVTFVHI-RIAAKUTSLVPKGL---- 238
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 231 RLTEGLTFQGLNSLEVLKLRQNNISK--LTDQAFWGLSKMHVLEYSVENVSGSLY 288
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 239 PPTLLELHDYNNKISVLEDFPKRYKELQRLGIGNKTTDIENGSLANIIPRVREIHLNN 298
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 289 LTAHQHLQHLNNSIAKIRHKGWFCQKHELVLFSNNLTRDLESLSLVRLSHN 348
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 299 KLKKIPSG-LPELKYLIQITFLHNSIARVGVNDFCTVPKMKKSLYSAISLFPNNPVK 354
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
349 SISHAFGAFKGLRSRVLDLDHNRISGT-TEDTSGAFSGLEFG-HSKLTLFGMKIK 403
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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1  RESULT 38
2  US-08-442-063A-33
3  ; Sequence 33, Application US/08442063A
4  ; Patent No. 5705609
5  ; GENERAL INFORMATION:
6  ; APPLICANT: RUOSLAHTI, ERKKI I.
7  ; APPLICANT: PIERSCHACHER, MICHAEL D.
8  ; APPLICANT: CARDENAS, JOSE
9  ; APPLICANT: CRAIG, WILLIAM
10 ; APPLICANT: MULLEN, DANIEL G.
11 ; TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
12 ; TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
13 ; NUMBER OF SEQUENCES: 62
14 ; CORRESPONDENCE ADDRESS:
15 ; ADDRESSEE: CAMPBELL AND FLORES
16 ; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
17 ; CITY: SAN DIEGO
18 ; STATE: CALIFORNIA
19 ; COUNTRY: UNITED STATES
20 ; ZIP: 92122
21 ; COMPUTER READABLE FORM:
22 ; MEDIUM TYPE: Floppy disk
23 ; COMPUTER: IBM PC compatible
24 ; OPERATING SYSTEM: PC-DOS/MS-DOS
25 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
26 ; CURRENT APPLICATION DATA:
27 ; APPLICATION NUMBER: US/08/442.063A
28 ; FILING DATE: 16-MAY-1995
29 ; CLASSIFICATION: 514
30 ; PRIOR APPLICATION DATA:
31 ; APPLICATION NUMBER: US 07/865,652
32 ; FILING DATE: 03-APR-1992
33 ; ATTORNEY/AGENT INFORMATION:
34 ; NAME: CAMPBELL, CATHRYN A.
35 ; REGISTRATION NUMBER: 31,815
36 ; REFERENCE/DOCKET NUMBER: P-LA 1454
37 ; TELECOMMUNICATION INFORMATION:
38 ; TELEPHONE: 619-535-9001
39 ; TELEFAX: 619-535-8949
40 ; INFORMATION FOR SEQ ID NO: 33:
41 ; SEQUENCE CHARACTERISTICS:
42 ; LENGTH: 96 amino acids
43 ; TYPE: amino acid
44 ; TOPOLOGY: linear
45 ; MOLECULE TYPE: protein

```

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US-08-442-063A-33

Query Match                12.9%; Score 256.5; DB 1; Length 96;
Best Local Similarity      54.8%; Pred. No. 4.1e-18;
Matches 51; Conservative 13; Mismatches 28; Indels 1; Gaps

QY 50 DEDNSLPTREPSRHFFPDLFPWCPCGCGCYSRVHVCSDLGTSVPTNIPFDTRMLDLQ 109
   || : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3 DEASIGIP-EVPDRDRDFEPLSGVPCPRCQCCHLRVQVCSDLGDKVKPKDLPPDTLLDQ 61
   || : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 110 NNKIKETKENDFGKLTSLYGLIILNNKLTKIHP 142
   ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |
Db 62 NNKITEKDGDFKKNLKNLHALLVNNKISKVSP 94
   ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |

RESULT 39
US-08-986-485-6
; Sequence 6, Application US/08986485
; Patent No. 6046030
; GENERAL INFORMATION:
; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,485
; FILING DATE: 08-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/059,448
; FILING DATE: 22-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-986-485-6

```

[illegible]


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Db 39 PACPAACVCSYDDADELSVFCSSRNLRTRPDGVPGGTQALWLDGNNLSVPPAAAFQNL 98
QY 126 SLYGLILNNKLTTHPKAFATTKLRLRLYLSHNLSEIPLNL---PKSLAELRIHENKV 182
Db 99 SLGFLNLQGGGLSLEPQALLGLENLCHLHLERNQLRSALGTFAITPALASGLSNRL 158
QY 183 KKIQKDTFKGMNALHVLMSANPLDNNGIEP-GAFEGVTVFHIRIAEAKLTSVPKGLPPT 241
Db 159 SRLEDGLFEGLSLWDLNLGWSL---AVLPDAAFRGL-----GS 195
QY 242 LLEHLNDYKISTVELEDFKRYKELQRLGLGNKKTIDENGSLANIPRVREITHLENNK 301
Db 196 LRELVLGNRLAYLQPALFSGLAELRELDLSNALRAIKANVFVQLPRLOKLYLDRLN 255
QY 302 KI-PSGLPELKYLIIFLHNSIARVGNDFCPTVPMKKSLSAISLFPNNPVKYMOP 360
Db 256 AVAPGAFLGLKALRWLDLSHNRVAGL-LEDTPFGLGLR-----VLRSLHNAIA--SLRP 307
QY 361 ATFRCLVSRMSVOLGN 376
Db 308 RTFKDLHFLLEELQLGH 323

```

RESULT 42

```

US-08-473-089-49
; Sequence 49, Application US/08473089
; Patent No. 6342368
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,089
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 605 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Insulin-like growth factor binding
; protein complex, Fig. 32
; INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-473-089-49

```

Query Match 12.3%; Score 246; DB 4; Length 605;
 Best Local Similarity 25.3%; Pred. No. 6.8e-16;
 Matches 80; Conservative 61; Mismatches 133; Indels 42; Gaps 9;

```

QY 72 PWCPPGCOCY-----SRVHCSDGLTSTVPTNIPFOTRMLDLQNNKIKEIKENDEKGLT 125
Db 39 PACPAACVCSYDDADELSVFCSSRNLRTRPDGVPGGTQALWLDGNNLSVPPAAAFQNL 98
QY 126 SLYGLILNNKLTTHPKAFATTKLRLRLYLSHNLSEIPLNL---PKSLAELRIHENKV 182
Db 99 SLGFLNLQGGGLSLEPQALLGLENLCHLHLERNQLRSALGTFAITPALASGLSNRL 158
QY 183 KKIQKDTFKGMNALHVLMSANPLDNNGIEP-GAFEGVTVFHIRIAEAKLTSVPKGLPPT 241
Db 159 SRLEDGLFEGLSLWDLNLGWSL---AVLPDAAFRGL-----GS 195
QY 242 LLEHLNDYKISTVELEDFKRYKELQRLGLGNKKTIDENGSLANIPRVREITHLENNK 301
Db 196 LRELVLGNRLAYLQPALFSGLAELRELDLSNALRAIKANVFVQLPRLOKLYLDRLN 255
QY 302 KI-PSGLPELKYLIIFLHNSIARVGNDFCPTVPMKKSLSAISLFPNNPVKYMOP 360
Db 256 AVAPGAFLGLKALRWLDLSHNRVAGL-LEDTPFGLGLR-----VLRSLHNAIA--SLRP 307
QY 361 ATFRCLVSRMSVOLGN 376
Db 308 RTFKDLHFLLEELQLGH 323

```

RESULT 43

```

US-08-487-072A-49
; Sequence 49, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,072A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 605 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Insulin-like growth factor binding
; protein complex, Fig. 32
; INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-487-072A-49

```

Query Match 12.3%; Score 246; DB 4; Length 605;

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,448
FILING DATE: 22-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70264
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-986-485-8

Query Match 12.0%; Score 239; DB 3; Length 180;
Best Local Similarity 25.6%; Pred. No. 5.6e-16;
Matches 58; Conservative 43; Mismatches 58; Indels 68; Gaps 3;

Qy 74 CPQCQYRVHCSDGLTSVPTNIPDTRMLDQNNKIKEIKENDPKGLTSLYGLILN 133
Db 5 CPSCLCFRTVCMHLLLEAVPAVAP-QTSILDRLFRNIREIQCAFRRRLNLTLLN 63
Qy 134 NNKLTTHPKAFLTTKKRLRLYLHSHNQLSEIPLNPKSLAELRIHENKVKIKQKDTFRGM 193
Db 64 NNQIKRIPSGAFEDLEMLKYL-----YKNEIOSIDRQAFGL 102
Qy 194 NALHVLMSANLNDNNGIEGAFEGVTFHRIAEAKLTSVPKGLPPTLLEHLHDYNKIS 253
Db 103 ASLE-----QYLHFNQTE 116
Qy 254 TVELEDFKRYKELQRLGIGNKKTIDTENGSLANIPRVREIHLNKKL 300
Db 117 TLPDPSQHLPKLERLELHNRRITHLVPGTFNHLMSKRLRDSNTL 163

RESULT 47
US-08-985-335-3
Sequence 3, Application US/08985335
Patent No. 6080847
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LATRUT02
CLONE: 1352286
US-08-985-335-3

Query Match 11.8%; Score 236; DB 3; Length 440;
Best Local Similarity 24.9%; Pred. No. 4.2e-15;
Matches 74; Conservative 52; Mismatches 117; Indels 54; Gaps 7;

Qy 78 CQCYS-----RVHCSDGLTSVPTNIPDTRMLDQNNKIKEIKENDPKGLTSLYGLILN 133
Db 54 CDVYTYLHEKYLDCQERKLVYLPQWQDQLHMLLARNKIRTLKNNMFSKFKKLSLDLQ 113
Qy 134 NNKLTTHPKAFLTTKKRLRLYLHSHNQLSEIPLNPKSLAELRIHEN-----180
Db 114 ONEISKIESAFGLKLTLLQHNQIKVLTVEEVIYTP-LLSYRLYDNPWHCTCEIE 172
Qy 181 -----KVKIKQKDTFRGMALHVLMSANLNDNNGIEP-----213
Db 173 TLISMLQIPNRNLGNVAKCESPOEQKNKKLQIKSEQLCNEEQQLDPKQVSGRPVI 232
Qy 214 -----GAFEGVTFHRIAEAK---LTSVPKGLPPTLLEHLHDYNKISVLEDFKRYKE 265
Db 233 KPEVDSTFCHNYVFPITLDCRKRKLKVPNNIPDPDIVKLDLSYNKINOLRPKEFEDVHE 292
Qy 266 LORLGLGNKKTIDTENGSLANIPRVREIHLNKKLKKIPSG-LPELKYLIQIIFLHNS 321
Db 293 LKKLNLSSNGIEFIDPAFLGLTHLELDLSNNSLQNFQVLEDFLKLWLDRN 349

RESULT 48
US-09-410-372-3
Sequence 3, Application US/09410372
Patent No. 6281334
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:

ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0421 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 440 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: LATRUT02
 CLONE: 1352286
 US-09-410-372-3

Query Match 11.8%; Score 236; DB 4; Length 440;
 Best Local Similarity 24.9%; Pred. No. 4.2e-15;
 Matches 74; Conservative 52; Mismatches 117; Indels 54; Gaps 7;
 QY 78 CQCY----RVVHCSDLGTSVPTNIPDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
 Db 54 CDVYTYLHEKYLDCQERKLVYVLPQWQDQLHMLLARKNKIRTLKNNMFSEKFKLSLDLQ 113
 QY 134 NKKLTIIHPKAFITTKKRLRYLSHNLQ-----SEIPLNPKSLAELRIHEN----- 180
 Db 114 ONEISKIESEAFGLNKLITLLQHQIKVLTEEVFIPT-LLSVRLYDNPWCTCEIE 172
 QY 181 -----KVKIKIODEKGMNALHVLMSANPLDNGIEP----- 213
 Db 173 TLISMLQIPRNGLNYAKCESPQKKNKLRQIKSEQLCNEEKEQLDPQVSGRPPI 232
 QY 214 -----GAFEGVTVFHRIAEAK---LTSVPKGLPPTLELHLDYNKISTVELEDFKRYKE 265
 Db 233 KPEVDSTFCHNVFPIQTLDCRKEKLVKVPNNIPDIVKLDLSYKINQLRPFEDVHE 292
 QY 266 LQRLGIGNNKITDIENGSLANIPRVREIHLNKKLKIIPSG-LPELYLOIIFLHSN 321
 Db 293 LKRLNLSNGIEFIDPAFLGLTHLELDLSNNSLQNFQVLEDDLYFLKLLWRDN 349

RESULT 49

PCT-US91-09055-4
 Sequence 4, Application PC/TUS9109055
 GENERAL INFORMATION:
 APPLICANT: Rothberg, Jonathan Marc and Artavanis-Tsakonas, Spyridon
 TITLE OF INVENTION: Purified SLIT protein and Sequence Elements Thereof
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Yale University
 ADDRESSEE: Office of Cooperative Research
 STREET: 246 Church Street
 CITY: Suite 401
 CITY: New Haven
 STATE: Connecticut
 COUNTRY: USA
 ZIP: 06510
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 6.0.5
 SOFTWARE: Microsoft Word 4.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/09055
 FILING DATE: 19911127
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/624,135
 FILING DATE: 7-DEC-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Barth, Richard J.

REGISTRATION NUMBER: 28,180
 REFERENCE/DOCKET NUMBER: 900964/RSB
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 972-1400
 TELEFAX: (212) 370-1622
 TELETYPE: 236268
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 224 amino acids
 TYPE: AMINO ACIDS
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Flank-LRR-Flank 2
 LOCATION: 1 to 224
 IDENTIFICATION METHOD: similarity to other Flank-LRR-
 OTHER INFORMATION: mediates adhesive events
 PCT-US91-09055-4

Query Match 11.1%; Score 222; DB 5; Length 224;
 Best Local Similarity 22.3%; Pred. No. 3.8e-14;
 Matches 69; Conservative 49; Mismatches 89; Indels 102; Gaps 8;
 QY 74 CPGCQCYSRVHCSDLGTSVPTNIPDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
 Db 1 CPHPCRCADGIVDCREKSLTSVPVTLDPDITDVRLEQNF----- 40
 QY 134 NKKLTIIHPKAFITTKKRLRYLSHNLQSEI---PLNLPKSLAELRIHENKVKIKIODETF 190
 Db 41 -----TELPKPSFSSPRRLRIDLSNNISRIADHLSGLKQLTTLVLYGNKIKDLPSSGVF 96
 QY 191 KGMNALHVLMSANPLDNGIEPCGAFEGVTVFHRIAEAKLTSVPKGLPPTLELHLDY 250
 Db 97 KGLGSLRLLLNA-----N 110
 QY 251 KISTVELEDFKRYKELQRLGIGNNKITDIENGSLANIPRVREIHLNKKLKIIPSGLP-- 308
 Db 111 EITCIRKDAFRDLHLSLSLLSYDNNISQSLANGTDFDAMKSMKTVHLAKN-----PFI 161
 QY 309 ---ELKYLIQIIFLHSNLSIARVGVNDFCTVPKMKKSLYSALSLENPNPKYKWEQATFRC 365
 Db 162 CDCNLRL-ADYLHKNPIETSGAR--CESPKRMHRR-----RIESLREEKFKC 206
 QY 366 VLRSMSVOL 374
 Db 207 SWGELRMKL 215

RESULT 50

US-09-232-160-17
 Sequence 17, Application US/09232160
 Patent No. 6368794
 GENERAL INFORMATION:
 APPLICANT: Steve Daniel
 APPLICANT: James Gilmore
 APPLICANT: Susan G. Stuart
 APPLICANT: Laura Stuve
 TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
 FILE REFERENCE: PA-0003 US
 CURRENT APPLICATION NUMBER: US/09/232,160
 CURRENT FILING DATE: 1999-01-15
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: PERL Program
 SEQ ID NO 17
 LENGTH: 298
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: -
 OTHER INFORMATION: 159452
 US-09-232-160-17

Query Match 10.7%; Score 212.5; DB 4; Length 298;

Search completed: January 24, 2003, 12:27:03
Job time : 24 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 24, 2003, 12:26:46 ; Search time 12 Seconds
(without alignments)
637.306 Million cell updates/sec

Title: US-09-944-457-2
Perfect score: 1992
Sequence: 1 MKEYVLLFLALCSAKPFS.....PATFRCLVSRMSVOLGNFGM 379

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1992	100.0	379	9	US-09-944-413-2
2	1992	100.0	379	9	US-09-944-413-2
3	1992	100.0	379	9	US-09-944-896-2
4	1992	100.0	379	9	US-09-944-944-2
5	1992	100.0	379	9	US-09-944-907-2
6	1992	100.0	379	9	US-09-944-929-2
7	1992	100.0	379	9	US-10-028-072-328
8	1992	100.0	379	10	US-09-866-028-2
9	1992	100.0	379	10	US-09-944-449-2
10	1992	100.0	379	10	US-09-944-457-2
11	1992	100.0	379	10	US-09-944-862-2
12	1992	100.0	379	10	US-09-945-587-2
13	1992	100.0	379	10	US-09-945-015-2
14	1992	100.0	379	10	US-09-944-396-2
15	1992	100.0	379	10	US-09-944-097-2
16	1992	100.0	379	10	US-09-944-432-2
17	1992	100.0	379	10	US-09-943-762-2
18	1992	100.0	379	10	US-09-944-654-2
19	1992	100.0	379	10	US-09-943-851A-2

20	406.5	20.4	155	10	US-09-925-301-1561	Sequence 1561, Ap
21	393	19.7	353	10	US-09-925-301-980	Sequence 980, App
22	366	18.4	421	9	US-10-028-072-302	Sequence 302, App
23	363.5	18.2	674	9	US-10-028-072-36	Sequence 36, Appl
24	331.5	16.6	623	10	US-09-764-870-276	Sequence 276, App
25	331.5	16.6	649	9	US-10-063-547-132	Sequence 132, App
26	331.5	16.6	649	9	US-10-004-551-6	Sequence 6, Appli
27	331.5	16.6	649	9	US-10-174-590-384	Sequence 384, App
28	331.5	16.6	649	9	US-10-176-758-384	Sequence 384, App
29	331.5	16.6	649	9	US-10-063-616-132	Sequence 132, App
30	331.5	16.6	649	9	US-10-175-737-384	Sequence 384, App
31	331.5	16.6	649	12	US-10-006-867-132	Sequence 132, App
32	331.5	16.6	649	12	US-10-052-586-384	Sequence 384, App
33	329	16.5	642	9	US-10-028-072-370	Sequence 370, App
34	323	16.2	415	10	US-09-925-301-1192	Sequence 1192, Ap
35	313.5	15.7	660	9	US-09-905-291A-28	Sequence 28, Appl
36	313.5	15.7	660	9	US-10-066-500-115	Sequence 115, App
37	313.5	15.7	660	9	US-09-902-853-28	Sequence 28, Appl
38	313.5	15.7	660	9	US-09-907-824-28	Sequence 28, Appl
39	313.5	15.7	660	9	US-09-907-841-28	Sequence 28, Appl
40	313.5	15.7	660	9	US-09-904-011-28	Sequence 28, Appl
41	313.5	15.7	660	9	US-10-028-072-350	Sequence 350, App
42	313.5	15.7	660	10	US-09-909-320-28	Sequence 28, Appl
43	313.5	15.7	660	10	US-09-909-088B-28	Sequence 28, Appl
44	313	15.7	1480	12	US-10-011-064-5	Sequence 5, Appli
45	309	15.5	1523	9	US-10-174-590-290	Sequence 290, App
46	309	15.5	1523	9	US-10-176-758-290	Sequence 290, App
47	309	15.5	1523	9	US-10-175-737-290	Sequence 290, App
48	309	15.5	1523	12	US-10-011-064-2	Sequence 2, Appli
49	309	15.5	1523	12	US-10-052-586-290	Sequence 290, App
50	304.5	15.3	513	9	US-10-063-547-124	Sequence 124, App

ALIGNMENTS

RESULT 1

US-09-944-413-2
; Sequence 2, Application US/09944413
; Patent No. US2002015600A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,413
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425

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Dd	61	PRSHFFPFDELPMCPFGQCYSRVYHVCHSGDGLTSVPNTIPFDTRMLDLQNKKIKEIKEND	120											
Qy	121	FKGTSLYGLTLNNKLTKHPKAFLTTKKLRRLYLHSNOLSEIPLMKSLAELRIHEN	180											
Dd	121	FKGTSLYGLTLNNKLTKTHPKAFLTTPKKLRRYLHSNOLSEIPLMKSLAELRIHEN	180											
Qy	181	KVKKIQRDKFMGNALHVLMSANPDNDNGIEPGAEGTVTFHIRIAEAKLTSPVGKLPP	240											
Dd	181	KVKKIQRDKTMGMNALHVLMSANPDNDNGIEPGAEGTVTFHIRIAEAKLTSPVGKLPP	240											
Qy	241	TLLLEHLDYNKISIVTELEDKFRYKEQLRIGLGNNKITDIENGSLANIPIVRREIHLENKKL	300											
Dd	241	TLLLEHLDYNAKSIVTELEDFKRYKEQLRIGLGNNKITDIENGSLANIPIVRREIHLENKKL	300											
Qy	301	KKIPSGLPELKYLQIIIFLHNSNSTARGVNDCFTVPKMCKSLYSALSINNPNKYWEMOP	360											
Dd	301	KKIPSGLPELKYLQIIFLHNSNSTARGVNDCFTVPKMCKSLYSALSINNPNKYWEMOP	360											
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US-09-944-403--2														
:	Sequence 2, Application US/09944403													
:	Patent No. US20020165143AI													
:	GENERAL INFORMATION:													
:	APPLICANT: Baker, Kevin													
:	APPLICANT: Baton, David													
:	APPLICANT: Eaton, Dan													
:	APPLICANT: Ferrara, Napoleone													
:	APPLICANT: Filvaroff, Ellen													
:	APPLICANT: Gerlitsen, Mary													
:	APPLICANT: Goddard, Audrey													
:	APPLICANT: Godowski, Paul													
:	APPLICANT: Grimaldi, Christopher													
:	APPLICANT: Gurney, Austin													
:	APPLICANT: Hillan, Kenneth													
:	APPLICANT: Kljavin, Ivar													
:	APPLICANT: Napier, Mary													
:	APPLICANT: Roy, Margaret													
:	APPLICANT: Tumas, Daniel													
:	APPLICANT: Wood, William													
:	TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME													
:	FILE REFERENCE: P2548PIC1													
:	CURRENT APPLICATION NUMBER: US/09/944.403													
:	CURRENT FILING DATE: 2001-09-26													
:	PRIOR APPLICATION NUMBER: 09/866, 028													
:	PRIOR FILING DATE: 2001-05-25													
:	PRIOR APPLICATION NUMBER: 60/067, 411													
:	PRIOR FILING DATE: December 3, 1997													
:	PRIOR APPLICATION NUMBER: 60/069, 334													
:	PRIOR FILING DATE: December 11, 1997													
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:	PRIOR APPLICATION NUMBER: 60/069, 278													
:	PRIOR FILING DATE: December 11, 1997													
:	PRIOR APPLICATION NUMBER: 60/069, 425													
:	PRIOR FILING DATE: December 12, 1997													
:	PRIOR APPLICATION NUMBER: 60/069, 696													
:	PRIOR FILING DATE: December 16, 1997													
:	PRIOR APPLICATION NUMBER: 60/069, 694													

	Query Match	100.0%;	Score 1992;	DB 9;	Length 379;
	Best Local Similarity	100.0%;	Pred. No. 2e-159;		
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Db	1	MKEYVLLFLALCSAKPFSPSHIALKNMMLKOMEDTDDDDDDDDDDDDDDNSLFPRTRE	60		
QY	61	PRSHFFPEDLFPMCFPGQCYSRVVHSCDGLTSTVPNTIPDFTRMLDLGNKKIKETKEND	120		
Db	61	PRSHFFPEDLFPMCFPGQCYSRVVHSCDGLTSTVPNTIPDFTRMLDLGNKKIKETKEND	120		

181	KVKIKQDTPFKGNALHVL	EMSNPLDNN	IEPGAFEGVTFV	HIRIAEAKLTSVPKGLPP	240
181	KVKIKQDTPFKGNALHVL	EMSNPLDNN	IEPGAFEGVTFV	HIRIAEAKLTSVPKGLPP	240
181	KVKIKQDTPFKGNALHVL	EMSNPLDNN	IEPGAFEGVTFV	HIRIAEAKLTSVPKGLPP	240
241	TLLELHDYNNKISTV	ELEDFKFKYKELORIGLGNKKIT	DIENGLSIANTIPRVRETHLENNKL	300	
241	TLLELHDYNNKISTV	ELEDFKFKYKELORIGLGNKKIT	DIENGLSIANTIPRVRETHLENNKL	300	
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301	KKIPSGLPPELKYLIQ	ITFLHSNSIARGVND	ECPTVPKMKKSLYSALSLENPNPKYVEMOP	360	
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RESULT 5

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US-09-944-907-2
; Sequence 2, Application US/09944907
; Publication No. US20020198147A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavini, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548PICI
; CURRENT APPLICATION NUMBER: US/09/944, 907
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 2
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo Sapien
; SEQ-09-944-907-2

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Query Match	100.0%;	Score 1992;	DB 9;	Length 379;
Best Local Similarity	100.0%;	Pred. No. 2e-159;		
Conservative	370.	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

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PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 2
LENGTH: 379
TYPE: PRT
ORGANISM: Homo sapien
S-09-944-944-2

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Query Match	100.0%;	Score 1992;	DB 9;	Length 379;
Best Local Similarity	100.0%;	Pred. No. 2e-159;		
Matches 379.	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

[illegible]

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Db 241 TLELHLDYKNIKSTVELEDFKRYKELQRLGLGNKNTIDENGSLANIPRVREIHLNNKL 300
QY 301 KKIPSGLPKLYLIQIIFLHNSNSTARVGVNDFCPTVPKMKKSLYSALSIFLNNPVKYWEMQ 360
Db 301 KKIPSGLPKLYLIQIIFLHNSNSTARVGVNDFCPTVPKMKKSLYSALSIFLNNPVKYWEMQ 360
QY 361 ATRFCVLSRMSVOLGNFGM 379
Db 361 ATRFCVLSRMSVOLGNFGM 379

RESULT 6
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; Sequence 2, Application US/09944929
; Publication No. US20020197612A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tamas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944, 929
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866, 028
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 2
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-929-2

Query Match 100.0%; Score 1992; DB 9; Length 379;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKMDTDDDDDDDDDDDDDDDDDDDDDDSLFPPTRE 60
Db 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKMDTDDDDDDDDDDDDDDDDDDDDDDSLFPPTRE 60
QY 61 PRSHFFPDLFPMCPFGCQCYRVVHGSDDLGLTSVPTNPDPFRMLDLQNNKIKELKEND 120
Db 61 PRSHFFPDLFPMCPFGCQCYRVVHGSDDLGLTSVPTNPDPFRMLDLQNNKIKELKEND 120
QY 121 FKGLTSLYGLTLNNKLTIKHPKAFLTTRKKRLYLHSHNQLSEIPLNLPKSLAEIRIHEN 180
Db 121 FKGLTSLYGLTLNNKLTIKHPKAFLTTRKKRLYLHSHNQLSEIPLNLPKSLAEIRIHEN 180
QY 181 KVKIKQDTEKGMNALHVLMSANPLDNGIEPGAEGVTVFHRIAEAKLTSVPKGLPP 240
Db 181 KVKIKQDTEKGMNALHVLMSANPLDNGIEPGAEGVTVFHRIAEAKLTSVPKGLPP 240
QY 241 TLELHLDYKNIKSTVELEDFKRYKELQRLGLGNKNTIDENGSLANIPRVREIHLNNKL 300
Db 241 TLELHLDYKNIKSTVELEDFKRYKELQRLGLGNKNTIDENGSLANIPRVREIHLNNKL 300
QY 301 KKIPSGLPKLYLIQIIFLHNSNSTARVGVNDFCPTVPKMKKSLYSALSIFLNNPVKYWEMQ 360

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Db 301 KKIPSGLPKLYLIQIIFLHNSNSTARVGVNDFCPTVPKMKKSLYSALSIFLNNPVKYWEMQ 360
QY 361 ATRFCVLSRMSVOLGNFGM 379
Db 361 ATRFCVLSRMSVOLGNFGM 379

RESULT 7
US-10-028-072-328
; Sequence 328, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028, 072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059836
; PRIOR FILING DATE: 1997-09-24
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062285
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062814
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/062816
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063082
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/063127
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063327

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1	PRIOR APPLICATION NUMBER: 60/083322
2	PRIOR FILING DATE: 1998-04-28
3	PRIOR APPLICATION NUMBER: 60/083545
4	PRIOR FILING DATE: 1998-04-29
5	PRIOR APPLICATION NUMBER: 60/084600
6	PRIOR FILING DATE: 1998-05-07
7	PRIOR APPLICATION NUMBER: 60/084627
8	PRIOR FILING DATE: 1998-05-07
9	PRIOR APPLICATION NUMBER: 60/084637
10	PRIOR FILING DATE: 1998-05-07
11	PRIOR APPLICATION NUMBER: 60/085149
12	PRIOR FILING DATE: 1998-05-12
13	PRIOR APPLICATION NUMBER: 60/085323
14	PRIOR FILING DATE: 1998-05-13
15	PRIOR APPLICATION NUMBER: 60/085338
16	PRIOR FILING DATE: 1998-05-13
17	PRIOR APPLICATION NUMBER: 60/085339
18	PRIOR FILING DATE: 1998-05-13
19	PRIOR APPLICATION NUMBER: 60/085579
20	PRIOR FILING DATE: 1998-05-15
21	PRIOR APPLICATION NUMBER: 60/085697
22	PRIOR FILING DATE: 1998-05-15
23	PRIOR APPLICATION NUMBER: 60/085704
24	PRIOR FILING DATE: 1998-05-15
25	PRIOR APPLICATION NUMBER: 60/086414
26	PRIOR FILING DATE: 1998-05-22
27	PRIOR APPLICATION NUMBER: 60/086430
28	PRIOR FILING DATE: 1998-05-22
29	PRIOR APPLICATION NUMBER: 60/087106
30	PRIOR FILING DATE: 1998-05-28
31	PRIOR APPLICATION NUMBER: 60/088026
32	PRIOR FILING DATE: 1998-06-04
33	PRIOR APPLICATION NUMBER: 60/088730
34	PRIOR FILING DATE: 1998-06-10
35	PRIOR APPLICATION NUMBER: 60/088741
36	PRIOR FILING DATE: 1998-06-10
37	PRIOR APPLICATION NUMBER: 60/088810
38	PRIOR FILING DATE: 1998-06-10
39	PRIOR APPLICATION NUMBER: 60/088858
40	PRIOR FILING DATE: 19/98-06-11
41	PRIOR APPLICATION NUMBER: 60/089532
42	PRIOR FILING DATE: 1998-06-17
43	PRIOR APPLICATION NUMBER: 60/089599
44	PRIOR FILING DATE: 1998-06-17
45	PRIOR APPLICATION NUMBER: 60/089907
46	PRIOR FILING DATE: 1998-06-18
47	PRIOR APPLICATION NUMBER: 60/089947
48	PRIOR FILING DATE: 1998-06-19
49	PRIOR APPLICATION NUMBER: 60/090349
50	PRIOR FILING DATE: 1998-06-23
51	PRIOR APPLICATION NUMBER: 60/090429
52	PRIOR FILING DATE: 1998-06-24
53	PRIOR APPLICATION NUMBER: 60/090445
54	PRIOR FILING DATE: 1998-06-24
55	PRIOR APPLICATION NUMBER: 60/090538
56	PRIOR FILING DATE: 1998-06-24
57	PRIOR APPLICATION NUMBER: 60/090863
58	PRIOR FILING DATE: 1998-06-26
59	PRIOR APPLICATION NUMBER: 60/091360
60	PRIOR FILING DATE: 1998-07-01
61	PRIOR APPLICATION NUMBER: 60/091519
62	PRIOR FILING DATE: 1998-07-02
63	PRIOR APPLICATION NUMBER: 60/091982
64	PRIOR FILING DATE: 1998-07-07

Query Match 100.0%: Score 1992: DB 9: Length 379;

Best Local Similarity 100.0%; Pred. No. 2e-159;

BEST LOCAL SIMILARITY: 100.0%; PRED: NO; ZC: 133,
Matches 379: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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Db .1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKMDMEDTDDDDDDDDDDDDNSLFP TRE 60

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Db 61 PRSHFFPDLFPMCPFGCCYSRVHCSDLGLTSVPTNIPEDTRMLDLQNNKIKEIKEND 120
QY 121 FKGLTSLYGLIILNNKLTTHPKAFLLTKKRLRLYLHNSHOLSEIPLNPKSLAEHLRIHEN 180
Db 121 FKGLTSLYGLIILNNKLTTHPKAFLLTKKRLRLYLHNSHOLSEIPLNPKSLAEHLRIHEN 180
QY 181 KVKIKQKDTFKGMNALHVLMSANPLDNGIEPGAEGVTVFHIRIAEAKLTSPKGLPP 240
Db 181 KVKIKQKDTFKGMNALHVLMSANPLDNGIEPGAEGVTVFHIRIAEAKLTSPKGLPP 240
QY 241 TLELHLDYNNKISTVELEDFKRYKELQRLGLGNKKTIDIEGSLANIIPRVREIHLNENKL 300
Db 241 TLELHLDYNNKISTVELEDFKRYKELQRLGLGNKKTIDIEGSLANIIPRVREIHLNENKL 300
QY 301 KKPISGLPELKYLIQIIFLHNSIARVGNDFCPTVPKMKKSLYSALSIFNPNVYKWMOP 360
Db 301 KKPISGLPELKYLIQIIFLHNSIARVGNDFCPTVPKMKKSLYSALSIFNPNVYKWMOP 360
QY 361 ATFRCLVLSRMSVOLGNFGM 379
Db 361 ATFRCLVLSRMSVOLGNFGM 379

RESULT 8

US-09-866-028-2
; Sequence 2, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 2
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-2

Query Match 100.0%; Score 1992; DB 10; Length 379;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKEYVLLFLALCSAKFFSFHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDDDNSLFPTRE 60
Db 1 MKEYVLLFLALCSAKFFSFHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDDDNSLFPTRE 60
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Db 61 PRSHFFPDLFPMCPFGCCYSRVHCSDLGLTSVPTNIPEDTRMLDLQNNKIKEIKEND 120
QY 121 FKGLTSLYGLIILNNKLTTHPKAFLLTKKRLRLYLHNSHOLSEIPLNPKSLAEHLRIHEN 180
Db 121 FKGLTSLYGLIILNNKLTTHPKAFLLTKKRLRLYLHNSHOLSEIPLNPKSLAEHLRIHEN 180

Db 121 FKGLTSLYGLIILNNKLTTHPKAFLLTKKRLRLYLHNSHOLSEIPLNPKSLAEHLRIHEN 180
QY 181 KVKIKQKDTFKGMNALHVLMSANPLDNGIEPGAEGVTVFHIRIAEAKLTSPKGLPP 240
Db 181 KVKIKQKDTFKGMNALHVLMSANPLDNGIEPGAEGVTVFHIRIAEAKLTSPKGLPP 240
QY 241 TLELHLDYNNKISTVELEDFKRYKELQRLGLGNKKTIDIEGSLANIIPRVREIHLNENKL 300
Db 241 TLELHLDYNNKISTVELEDFKRYKELQRLGLGNKKTIDIEGSLANIIPRVREIHLNENKL 300
QY 301 KKPISGLPELKYLIQIIFLHNSIARVGNDFCPTVPKMKKSLYSALSIFNPNVYKWMOP 360
Db 301 KKPISGLPELKYLIQIIFLHNSIARVGNDFCPTVPKMKKSLYSALSIFNPNVYKWMOP 360
QY 361 ATFRCLVLSRMSVOLGNFGM 379
Db 361 ATFRCLVLSRMSVOLGNFGM 379

RESULT 9

US-09-944-449-2
; Sequence 2, Application US/09944449
; Patent No. US20020102647A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,449
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998

[illegible]

[illegible]


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; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 2
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo Sapien

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US-09-945-015-2

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Query Match 100.0%; Score 1992; DB 10; Length 379;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKEYVLLFLALCSAKPFFSPSHALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDNSLPPTRE 60

QY 61 PRSHFFPDLFPMCPFCGCQYRVVHCSDGLTSVPTNIPFDTMRMLDLQNNKIKEIKEND 120
Db 61 PRSHFFPDLFPMCPFCGCQYRVVHCSDGLTSVPTNIPFDTMRMLDLQNNKIKEIKEND 120

QY 121 FKGLTSLYGLILNNKNTKTHPKAFLTKRLRLYLISHNOLSEIPLNPKSLAELRIHEN 180
Db 121 FKGLTSLYGLILNNKNTKTHPKAFLTKRLRLYLISHNOLSEIPLNPKSLAELRIHEN 180

QY 181 KVKKIQDTPKGMNALHVLMSANPLDNGIEGAFEGVTVFHRITAEAKLTSPVKGGLPP 240
Db 181 KVKKIQDTPKGMNALHVLMSANPLDNGIEGAFEGVTVFHRITAEAKLTSPVKGGLPP 240

QY 241 TLELHLHDYNNKISTVELEDFKRYKELQRLGLGNKNTIDIEGSLANIPRVREIHLNNKL 300
Db 241 TLELHLHDYNNKISTVELEDFKRYKELQRLGLGNKNTIDIEGSLANIPRVREIHLNNKL 300

QY 301 KKIFSGLPKLYLQIIFLHNSNARVGNDFCTVPKMKKSLYSATSLFNNPKYKWMQP 360
Db 301 KKIFSGLPKLYLQIIFLHNSNARVGNDFCTVPKMKKSLYSATSLFNNPKYKWMQP 360

QY 361 ATRFCVLRSMSVQLGNFGM 379
Db 361 ATRFCVLRSMSVQLGNFGM 379

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RESULT 14

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US-09-944-396-2
; Sequence 2, Application US/09944396
; Patent No. US20020132981A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavini, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548PICI
; CURRENT APPLICATION NUMBER: US/09/944,396
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
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; PRIOR APPLICATION NUMBER: 60/069,696
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; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999

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; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020132981A1e1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020132981A1e1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 2
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-396-2

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Query Match      100.0%; Score 1992; DB 10; Length 379;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFTPRE 60
Db 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFTPRE 60

QY 61 PRSHFFPDLPMCPFGCQCSRVVHCSDLGTSVPTNIPDTRMLDLQNNKIKEIKEND 120
Db 61 PRSHFFPDLPMCPFGCQCSRVVHCSDLGTSVPTNIPDTRMLDLQNNKIKEIKEND 120

QY 121 FKGLTSLYGLILNNKLTKEHPKAFLLTKLRLRLYLSHNQLSETPLNPKSLAELRIHEN 180
Db 121 FKGLTSLYGLILNNKLTKEHPKAFLLTKLRLRLYLSHNQLSETPLNPKSLAELRIHEN 180

QY 181 KVKTKQDFTFGMNAHVLEMSANPLDNGGIEPGAFEGSVTVFHIRIAEAKLTSVPKGLPP 240
Db 181 KVKTKQDFTFGMNAHVLEMSANPLDNGGIEPGAFEGSVTVFHIRIAEAKLTSVPKGLPP 240

QY 241 TLLEHLDYNNKISVLEDEFRYKELQRLGNNKITDIENGSLANTPRVREIHLNENKL 300
Db 241 TLLEHLDYNNKISVLEDEFRYKELQRLGNNKITDIENGSLANTPRVREIHLNENKL 300

QY 301 KKIPSGPELKYLOIFLHNSIARVGVNDFCTVPKMKKSLYSALSLENNPVKYWEMQP 360
Db 301 KKIPSGPELKYLOIFLHNSIARVGVNDFCTVPKMKKSLYSALSLENNPVKYWEMQP 360

QY 361 ATFRCLSRMSVQLGNFGM 379
Db 361 ATFRCLSRMSVQLGNFGM 379

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RESULT 15
US-09-944-097-2
; Sequence 2, Application US/09944097
; Patent No. US20020133675A1
; GENERAL INFORMATION:

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; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944, 097
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866, 028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/069, 334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069, 696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069, 694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069, 702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069, 870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069, 873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068, 017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070, 440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074, 086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074, 092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075, 945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112, 850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113, 296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146, 222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216, 021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218, 517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254, 311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020133675A1e1ember 30, 1999

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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US2002013367/5alembler 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 2
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-944-097-2

Query Match 100.0%; Score 1992; DB 10; Length 379;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKEYVLLFLALCSAKPFFSPSHALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDNSLPPTRE 60
DB 1 MKEYVLLFLALCSAKPFFSPSHALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDNSLPPTRE 60

QY 61 PRSHFFFDLPPMPCFCQCQYRVHCSGLGTSVPTNPFDRLMDLQNNKIKEIKEND 120
DB 61 PRSHFFFDLPPMPCFCQCQYRVHCSGLGTSVPTNPFDRLMDLQNNKIKEIKEND 120

QY 121 FKGLTSLYGLTLNNKLTTHKRAFTTTKKRLRLYLSHNSLSTIPNLNPKSLAELRHEN 180
DB 121 FKGLTSLYGLTLNNKLTTHKRAFTTTKKRLRLYLSHNSLSTIPNLNPKSLAELRHEN 180

QY 181 KVKIKQDTPKGMNHLVLEMSANPLDNGIEPCAFEGVTVFHRTAEAKLTSPVKGGLPP 240
DB 181 KVKIKQDTPKGMNHLVLEMSANPLDNGIEPCAFEGVTVFHRTAEAKLTSPVKGGLPP 240

QY 241 TLELHLDYNNKISTVELEDKRYKELQRLGNNKTTDIENGSLANIPRVREITHLENNKL 300
DB 241 TLELHLDYNNKISTVELEDKRYKELQRLGNNKTTDIENGSLANIPRVREITHLENNKL 300

QY 301 KKIPSGLPKYLQIIFLHNSIARVGVNDFCTVPKMKKSLYSALSFNNPVKYWPMQP 360
DB 301 KKIPSGLPKYLQIIFLHNSIARVGVNDFCTVPKMKKSLYSALSFNNPVKYWPMQP 360

QY 361 ATFRCVLSRMSVQLNGFGM 379
DB 361 ATFRCVLSRMSVQLNGFGM 379

RESULT 16
US-09-944-432-2
; Sequence 2, Application US/09944432
; Patent No. US20020142419A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,432
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020142419A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020142419A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
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; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 2
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-943-762-2

Query Match          100.0%; Score 1992; DB 10; Length 379;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKEVVLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDNSLPPTRE 60
Db 1 MKEVVLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDNSLPPTRE 60

Qy 61 PRSHFFFDLPMPFCGQCYSRVVHCHSDGLTSVPTNIPFDTRMLDLQNNKIKEIKEND 120
Db 61 PRSHFFFDLPMPFCGQCYSRVVHCHSDGLTSVPTNIPFDTRMLDLQNNKIKEIKEND 120

Qy 121 FKGLTSLYGLILNNKLTJTKHPKAFLTTKLRLRLYLSHNSLSEIPLNPKSLAELRIHEN 180
Db 121 FKGLTSLYGLILNNKLTJTKHPKAFLTTKLRLRLYLSHNSLSEIPLNPKSLAELRIHEN 180

Qy 181 KVKIKQDTEFGKMAHVLNSANPLDNGIEPGAFSGVTFVHRIAEAKLTSPVKGLPP 240
Db 181 KVKIKQDTEFGKMAHVLNSANPLDNGIEPGAFSGVTFVHRIAEAKLTSPVKGLPP 240

Qy 241 TLLEHLHDYNNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPTVRYREIHLNKKL 300
Db 241 TLLEHLHDYNNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPTVRYREIHLNKKL 300

Qy 301 KKIISGLPELKYLIQIIFLHNSIARVGVNDFCPTVPKMKSLYSALSLFNNPKYWMQ 360
Db 301 KKIISGLPELKYLIQIIFLHNSIARVGVNDFCPTVPKMKSLYSALSLFNNPKYWMQ 360

Qy 361 ATRFCVLSRMSVQLGNFGM 379
Db 361 ATRFCVLSRMSVQLGNFGM 379

RESULT 18
US-09-944-654-2
; Sequence 2, Application US/09944654
; Patent No. US20020142959A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
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US-09-925-301-1561
Query Match      20.4%; Score 406.5; DB 10; Length 155;
Best Local Similarity 50.3%; Pred. No. 3.3e-27;
Matches 77; Conservative 33; Mismatches 42; Indels 1; Gaps 1;

QY 176 RIHNKVYKIQDFTFGMNAHVLMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSV 234
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 RAHENETTKVRKYTFNGNLNOMIVIELGTNPDKSSGIEGAFQGCKKLVSIRIADTNITSI 60

QY 235 PKGLPPTLLEHLHDYNKISTVELEDPKRYELORLGLGNKKITDIENGSLANIIPRVREIH 294
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 PQGLPPSLTEHLHDGNKRISVDAAASUGLNLAKLGLSFNISISAVDNGSLANTPHLRRELH 120

QY 295 LENNKLKIPSGLPKELYGIIFLSHSNSIARVG 327
    |:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 LDNNKLTRVPGGLQSIXYXGGYLHNHHISVVG 153

RESULT 21
US-09-925-301-980
; Sequence 980, Application US/09925301
; Patent No. US2002005308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 980
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (333)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (346)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-980

Query Match      19.7%; Score 393; DB 10; Length 353;
Best Local Similarity 31.7%; Pred. No. 1.3e-25;
Matches 102; Conservative 70; Mismatches 128; Indels 22; Gaps 10;

QY 66 FPDLF----PMCFPGQC---YSRVVHCSDLGTVTNPDPTRMLDLONNKIKEIKE 118
    ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
Db 40 FPLSIYGQSSPNCAPECNPCSPSAMCYDELKLVPM-VPPGIKLYLRNNIDHIDE 98

QY 119 NDPFGLTSLXYLIILNNKL--TKTHPKAFLTTKRLRLLSHNOLSEPLNPKSLAE LR 176
    |:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 99 KAENVVTDLQWLIDLDHLLNSKIKGRVFSKLGKOLKLHLHNNLTLSVGPLPSKLDQL 158

QY 177 IHENKVKKIORDFKGMNALHVLEMSANPDNDNGIEPGAEGV-TVFHIRIAEAKLTSVP 235
    :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 159 LTHNKITKL--GSFEGVLNLTFFIHLQHNRUKEDAVS-AAPKGLASLEVLDLSFNQIARLP 215

QY 236 KGLPPTLLEHLHDYNKISTVELEDPKRYELORLGLGNKKITDTE-NGSLANIIPRVREIH 294
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 216 SGLPVSLTLTYLDONNKISINPIDXEYFKRFNALQYLRLSHNELADSGIPGNSFVSSLVELD 275

QY 295 LENNKLKIPSGLPKELK--YLIIFIHLSNSIARVGVNDFCPTVPKMKSLSYSAISLFNFP 352
    ||||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 276 LSYNKNKITPTVNLENLYLEV-----NQLEKFDIKSFCKILGLPLSYSKTKHLRLDG NR 330

QY 353 VKYWEMQPATPRFCVLSRMSVOL 374

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Db 331 ISXTSLPDMYECIRXANEVTL 352

RESULT 22

US-10-028-072-302

Sequence 302, Application US/10028072

Publication No. US20030004311A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvarcoff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang

TITLE OF INVENTION:

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/028, 072

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059115

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059122

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059352

PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/059588

PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/059836

PRIOR FILING DATE: 1997-09-24

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/062285

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/062287

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/062814

PRIOR FILING DATE: 1997-10-24

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PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063045

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063082

PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/063127

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063327

PRIOR FILING DATE: 1997-10-27

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PRIOR FILING DATE: 1997-10-27

PRIOR APPLICATION NUMBER: 60/063550

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PRIOR FILING DATE: 1997-10-29

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PRIOR FILING DATE: 1997-10-29

PRIOR APPLICATION NUMBER: 60/063755

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064248

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/064809

PRIOR FILING DATE: 1997-11-07

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065846

PRIOR FILING DATE: 1997-11-17

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/066453

PRIOR FILING DATE: 1997-11-24

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PRIOR FILING DATE: 1997-11-24

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PRIOR FILING DATE: 1997-12-11

PRIOR APPLICATION NUMBER: 60/069694

PRIOR FILING DATE: 1997-12-16

PRIOR APPLICATION NUMBER: 60/072320

PRIOR FILING DATE: 1998-01-23

PRIOR APPLICATION NUMBER: 60/073612

PRIOR FILING DATE: 1998-02-04

PRIOR APPLICATION NUMBER: 60/074086

PRIOR FILING DATE: 1998-03-09

PRIOR APPLICATION NUMBER: 60/074092

PRIOR FILING DATE: 1998-02-09

PRIOR APPLICATION NUMBER: 60/077791

PRIOR FILING DATE: 1998-03-12

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/079294

PRIOR FILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 60/079663

PRIOR FILING DATE: 1998-02-27

PRIOR APPLICATION NUMBER: 60/079728

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/080165

PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: 60/081203

PRIOR FILING DATE: 1998-04-09

PRIOR APPLICATION NUMBER: 60/081229

PRIOR FILING DATE: 1998-04-09

PRIOR APPLICATION NUMBER: 60/081695

PRIOR FILING DATE: 1998-04-14

PRIOR APPLICATION NUMBER: 60/081817

PRIOR FILING DATE: 1998-04-15

PRIOR APPLICATION NUMBER: 60/081818

PRIOR FILING DATE: 1998-04-15

PRIOR APPLICATION NUMBER: 60/082999

PRIOR FILING DATE: 1998-04-24

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/083545

PRIOR FILING DATE: 1998-04-29

1 PRIOR APPLICATION NUMBER: 60/062816
2 PRIOR FILING DATE: 1997-10-24
3 PRIOR APPLICATION NUMBER: 60/063045
4 PRIOR FILING DATE: 1997-10-24
5 PRIOR APPLICATION NUMBER: 60/063082
6 PRIOR FILING DATE: 1997-10-31
7 PRIOR APPLICATION NUMBER: 60/063127
8 PRIOR FILING DATE: 1997-10-24
9 PRIOR APPLICATION NUMBER: 60/063327
10 PRIOR FILING DATE: 1997-10-27
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12 PRIOR FILING DATE: 1997-10-27
13 PRIOR APPLICATION NUMBER: 60/063550
14 PRIOR FILING DATE: 1997-10-28
15 PRIOR APPLICATION NUMBER: 60/063561
16 PRIOR FILING DATE: 1997-10-28
17 PRIOR APPLICATION NUMBER: 60/063704
18 PRIOR FILING DATE: 1997-10-29
19 PRIOR APPLICATION NUMBER: 60/063733
20 PRIOR FILING DATE: 1997-10-29
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26 PRIOR FILING DATE: 1997-10-17
27 PRIOR APPLICATION NUMBER: 60/064248
28 PRIOR FILING DATE: 1997-11-03
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30 PRIOR FILING DATE: 1997-11-07
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33 PRIOR APPLICATION NUMBER: 60/065846
34 PRIOR FILING DATE: 1997-11-17
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37 PRIOR APPLICATION NUMBER: 60/066453
38 PRIOR FILING DATE: 1997-11-24
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43 PRIOR APPLICATION NUMBER: 60/069212
44 PRIOR FILING DATE: 1997-12-11
45 PRIOR APPLICATION NUMBER: 60/069278
46 PRIOR FILING DATE: 1997-12-11
47 PRIOR APPLICATION NUMBER: 60/069334
48 PRIOR FILING DATE: 1997-12-11
49 PRIOR APPLICATION NUMBER: 60/069694
50 PRIOR FILING DATE: 1997-12-16
51 PRIOR APPLICATION NUMBER: 60/072320
52 PRIOR FILING DATE: 1998-01-23
53 PRIOR APPLICATION NUMBER: 60/073612
54 PRIOR FILING DATE: 1998-02-04
55 PRIOR APPLICATION NUMBER: 60/074086
56 PRIOR FILING DATE: 1998-02-09
57 PRIOR APPLICATION NUMBER: 60/074092
58 PRIOR FILING DATE: 1998-02-09
59 PRIOR APPLICATION NUMBER: 60/077791
60 PRIOR FILING DATE: 1998-03-12
61 PRIOR APPLICATION NUMBER: 60/078910
62 PRIOR FILING DATE: 1998-03-20
63 PRIOR APPLICATION NUMBER: 60/079294
64 PRIOR FILING DATE: 1998-03-25
65 PRIOR APPLICATION NUMBER: 60/079663
66 PRIOR FILING DATE: 1998-02-27
67 PRIOR APPLICATION NUMBER: 60/079728
68 PRIOR FILING DATE: 1998-03-27
69 PRIOR APPLICATION NUMBER: 60/080165
70 PRIOR FILING DATE: 1998-03-31
71 PRIOR APPLICATION NUMBER: 60/081203
72 PRIOR FILING DATE: 1998-04-09
73 PRIOR APPLICATION NUMBER: 60/081229

74 PRIOR FILING DATE: 1998-04-09
75 PRIOR APPLICATION NUMBER: 60/081695
76 PRIOR FILING DATE: 1998-04-14
77 PRIOR APPLICATION NUMBER: 60/081817
78 PRIOR FILING DATE: 1998-04-15
79 PRIOR APPLICATION NUMBER: 60/081818
80 PRIOR FILING DATE: 1998-04-15
81 PRIOR APPLICATION NUMBER: 60/082999
82 PRIOR FILING DATE: 1998-04-24
83 PRIOR APPLICATION NUMBER: 60/083322
84 PRIOR FILING DATE: 1998-04-28
85 PRIOR APPLICATION NUMBER: 60/083545
86 PRIOR FILING DATE: 1998-04-29
87 PRIOR APPLICATION NUMBER: 60/084600
88 PRIOR FILING DATE: 1998-05-07
89 PRIOR APPLICATION NUMBER: 60/084627
90 PRIOR FILING DATE: 1998-05-07
91 PRIOR APPLICATION NUMBER: 60/084637
92 PRIOR FILING DATE: 1998-05-07
93 PRIOR APPLICATION NUMBER: 60/085149
94 PRIOR FILING DATE: 1998-05-12
95 PRIOR APPLICATION NUMBER: 60/085323
96 PRIOR FILING DATE: 1998-05-13
97 PRIOR APPLICATION NUMBER: 60/085338
98 PRIOR FILING DATE: 1998-05-13
99 PRIOR APPLICATION NUMBER: 60/085339
100 PRIOR FILING DATE: 1998-05-13
101 PRIOR APPLICATION NUMBER: 60/085579
102 PRIOR FILING DATE: 1998-05-15
103 PRIOR APPLICATION NUMBER: 60/085697
104 PRIOR FILING DATE: 1998-05-15
105 PRIOR APPLICATION NUMBER: 60/085704
106 PRIOR FILING DATE: 1998-05-15
107 PRIOR APPLICATION NUMBER: 60/086414
108 PRIOR FILING DATE: 1998-05-22
109 PRIOR APPLICATION NUMBER: 60/086430
110 PRIOR FILING DATE: 1998-05-22
111 PRIOR APPLICATION NUMBER: 60/087106
112 PRIOR FILING DATE: 1998-05-28
113 PRIOR APPLICATION NUMBER: 60/088026
114 PRIOR FILING DATE: 1998-06-04
115 PRIOR APPLICATION NUMBER: 60/088730
116 PRIOR FILING DATE: 1998-06-10
117 PRIOR APPLICATION NUMBER: 60/088741
118 PRIOR FILING DATE: 1998-06-10
119 PRIOR APPLICATION NUMBER: 60/088810
120 PRIOR FILING DATE: 1998-06-10
121 PRIOR APPLICATION NUMBER: 60/088858
122 PRIOR FILING DATE: 1998-06-11
123 PRIOR APPLICATION NUMBER: 60/089532
124 PRIOR FILING DATE: 1998-06-17
125 PRIOR APPLICATION NUMBER: 60/089599
126 PRIOR FILING DATE: 1998-06-17
127 PRIOR APPLICATION NUMBER: 60/089907
128 PRIOR FILING DATE: 1998-06-18
129 PRIOR APPLICATION NUMBER: 60/089947
130 PRIOR FILING DATE: 1998-06-19
131 PRIOR APPLICATION NUMBER: 60/090349
132 PRIOR FILING DATE: 1998-06-23
133 PRIOR APPLICATION NUMBER: 60/090429
134 PRIOR FILING DATE: 1998-06-24
135 PRIOR APPLICATION NUMBER: 60/090445
136 PRIOR FILING DATE: 1998-06-24
137 PRIOR APPLICATION NUMBER: 60/090538
138 PRIOR FILING DATE: 1998-06-24
139 PRIOR APPLICATION NUMBER: 60/090863
140 PRIOR FILING DATE: 1998-06-26
141 PRIOR APPLICATION NUMBER: 60/091360
142 PRIOR FILING DATE: 1998-07-01
143 PRIOR APPLICATION NUMBER: 60/091519
144 PRIOR FILING DATE: 1998-07-02
145 PRIOR APPLICATION NUMBER: 60/091982
146 PRIOR FILING DATE: 1998-07-07


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Query Match      18.2%; Score 363.5; DB 9; Length 674;
Best Local Similarity 32.7%; Pred. No. 9.1e-23;
Matches 92; Conservative 51; Mismatches 105; Indels 33; Gaps 7;

QY 74 CPGGQCYSRVVHCSDGLTSTVPTNIPDTRMLDQNNKKEIKENDFKGLTSLYGLILN 133
Db 54 CPGVCRCDNGFYCNDRLTSTPAIDPDATTLYLQNNQI-----N 94

QY 134 NKKLTTHPKAFITTKLRRLYLSHNQLSEITPLNPKSLAEIRHENKVKIKQDTPFGM 193
Db 95 NAGI-----PSDLKLLKVERIYHNSLDEFTNPKYVKELHLQENNTITYDSLSKI 150

QY 194 NALHVLMSANPLDNGIEPGAF-EGVTVFHIRIAEAKLTSVPKGLPTLLEHLHDYDKI 252
Db 151 PLEELHDDNSVTSVIEEAFADSKQKULFLSRNHLSSIPSGLPHTLEELRLDDNRI 210

QY 253 STVELEDFKRYKELQRLGLGNKKTID--IENGSLANIPRVREIHLNKKIKIPSGLP 310
Db 211 STIPLHAFKGLNSLRRLVLDGNLANQRIADDTFSLQNLITELSLVRNSLAAPPLNLP 269

QY 311 KYLQIIFLHNSIARVGVNDPCTVPKMKKSLYSALSIFNN 351
Db 270 AHLQKLYLDNAISHIPYN---TLAKMRE--LERLDLSNN 304

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RESULT 24
US-09-764-870-276
; Sequence 276, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PZ14
; CURRENT APPLICATION NUMBER: US/09764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 276
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-276

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Query Match      16.6%; Score 331.5; DB 10; Length 623;
Best Local Similarity 33.0%; Pred. No. 3.9e-20;
Matches 86; Conservative 37; Mismatches 111; Indels 27; Gaps 5;

QY 74 CPGGQCYSRVVHCSDGLTSTVPTNIPDTRMLDQNNKKEIKENDFKGLTSLYGLILN 133
Db 5 CPGVCRCDAGFYCNDRLTSTIPGIPEDATTLYLQNNQI-----N 45

QY 134 NKKLTTHPKAFITTKLRRLYLSHNQLSEITPLNPKSLAEIRHENKVKIKQDTPFGM 193
Db 46 NAGI-----PSDLKLLKVERIYHNSLDEFTNPKYVKELHLQENNTITYDSLSKI 101

QY 194 NALHVLMSANPLDNGIEPGAFEGVTVFHIR-IAEAKLTSVPKGLPTLLEHLHDYDKI 252
Db 102 PLEELHDDNSVSAVSIEEAGAFSDSNYRLFLSRNHLSTIPWGLPRTTEELRLDDNRI 161

QY 253 STVELEDFKRYKELQRLGLGNKKTIDENG--LANIPRVREIHLNKKIKIPSGLP 310
Db 162 STISSPSLQGLTSLKRLVLDGNLNNHGLGDKVFFNLVNLTELSELVRNSLTAAPVNLPGT 221

QY 311 KYLQIIFLHNSIARVGVNDP 331
Db 222 N-LRKLYLDQNHINRVPPNAF 241

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RESULT 25
US-10-063-547-132
; Sequence 132, Application US/10063547

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; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,547
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 132
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-547-132

```

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Query Match      16.6%; Score 331.5; DB 9; Length 649;
Best Local Similarity 33.0%; Pred. No. 4.1e-20;
Matches 86; Conservative 37; Mismatches 111; Indels 27; Gaps 5;

QY 74 CPGGQCYSRVVHCSDGLTSTVPTNIPDTRMLDQNNKKEIKENDFKGLTSLYGLILN 133
Db 31 CPGVCRCDAGFYCNDRLTSTIPGIPEDATTLYLQNNQI-----N 71

QY 134 NKKLTTHPKAFITTKLRRLYLSHNQLSEITPLNPKSLAEIRHENKVKIKQDTPFGM 193
Db 72 NAGI-----PSDLKLLKVERIYHNSLDEFTNPKYVKELHLQENNTITYDSLSKI 127

QY 194 NALHVLMSANPLDNGIEPGAFEGVTVFHIR-IAEAKLTSVPKGLPTLLEHLHDYDKI 252
Db 128 PLEELHDDNSVSAVSIEEAGAFSDSNYRLFLSRNHLSTIPWGLPRTTEELRLDDNRI 187

QY 253 STVELEDFKRYKELQRLGLGNKKTIDENG--LANIPRVREIHLNKKIKIPSGLP 310
Db 188 STISSPSLQGLTSLKRLVLDGNLNNHGLGDKVFFNLVNLTELSELVRNSLTAAPVNLPGT 247

QY 311 KYLQIIFLHNSIARVGVNDP 331
Db 248 N-LRKLYLDQNHINRVPPNAF 267

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RESULT 26
US-10-004-551-6
; Sequence 6, Application US/10004551
; Publication No. US20030004310A1
; GENERAL INFORMATION:
; APPLICANT: SHIMKETS, RICHARD A
; APPLICANT: FERNANDES, ELMA
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
; FILE REFERENCE: 15966-559
; CURRENT APPLICATION NUMBER: US/10/004,551
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 09/635,949
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-004-551-6

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Query Match      16.6%; Score 331.5; DB 9; Length 649;
Best Local Similarity 33.0%; Pred. No. 4.1e-20;
Matches 86; Conservative 37; Mismatches 111; Indels 27; Gaps 5;

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Db 248 N-LRKLYLQDNHINRVPNPF 267

RESULT 28
US-10-176-758-384
; Sequence 384, Application US/10176758
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 384
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-176-758-384

Query Match 16.6%; Score 331.5; DB 9; Length 649;
Best Local Similarity 33.0%; Pred. No. 4.1e-20;
Matches 86; Conservative 37; Mismatches 111; Indels 27; Gaps 5;

QY 74 CPFGCQYSRVHCSDLGTSVPTNIPDTRMLDQNNKIKEIKENDFKGLTSLYGLILN 133
Db 31 CPSCVRCDAFYCNDRFLTSIPTGIPEDATTLYLQNNQI-----N 71

QY 134 NNLKTIHPKAFITTKLRLRLYLSHNSLSEIPLNLPKSLAEIRIHENKVKIKQDFTKGM 193
Db 72 NAGI-----PSDLKLLKVERIYIYNSLDEFPNLPKYVKELHQLQENNIRITITDLSKI 127

QY 194 NALHVLMSANPLDNNNGIEPGAFEGVTVFHIR-IAEAKLTSVPKGLPPTLLELHLDYNKI 252
Db 128 PYLEELHLDNNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRI 187

QY 253 STVELEDFRYKELORLGLGNKKTIDENG--LANIPRVREIHLNENKLLKIPSGLP 310
Db 188 STISSPSLQGLTSLKRLVLDGNLNNHGLGDKVFFNLVNLTELSLRNSLTAAPVNLPGT 247

QY 311 KYLQIIFLHSNSIARVGNDF 331
Db 248 N-LRKLYLQDNHINRVPNPF 267

RESULT 29
US-10-063-616-132
; Sequence 132, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
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QY 74 CPFGCQYSRVHCSDLGTSVPTNIPDTRMLDQNNKIKEIKENDFKGLTSLYGLILN 133
Db 31 CPSCVRCDAFYCNDRFLTSIPTGIPEDATTLYLQNNQI-----N 71

QY 134 NNLKTIHPKAFITTKLRLRLYLSHNSLSEIPLNLPKSLAEIRIHENKVKIKQDFTKGM 193
Db 72 NAGI-----PSDLKLLKVERIYIYNSLDEFPNLPKYVKELHQLQENNIRITITDLSKI 127

QY 194 NALHVLMSANPLDNNNGIEPGAFEGVTVFHIR-IAEAKLTSVPKGLPPTLLELHLDYNKI 252
Db 128 PYLEELHLDNNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRI 187

QY 253 STVELEDFRYKELORLGLGNKKTIDENG--LANIPRVREIHLNENKLLKIPSGLP 310
Db 188 STISSPSLQGLTSLKRLVLDGNLNNHGLGDKVFFNLVNLTELSLRNSLTAAPVNLPGT 247

QY 311 KYLQIIFLHSNSIARVGNDF 331
Db 248 N-LRKLYLQDNHINRVPNPF 267

RESULT 27
US-10-174-590-384
; Sequence 384, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 384
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-174-590-384

Query Match 16.6%; Score 331.5; DB 9; Length 649;
Best Local Similarity 33.0%; Pred. No. 4.1e-20;
Matches 86; Conservative 37; Mismatches 111; Indels 27; Gaps 5;

QY 74 CPFGCQYSRVHCSDLGTSVPTNIPDTRMLDQNNKIKEIKENDFKGLTSLYGLILN 133
Db 31 CPSCVRCDAFYCNDRFLTSIPTGIPEDATTLYLQNNQI-----N 71

QY 134 NNLKTIHPKAFITTKLRLRLYLSHNSLSEIPLNLPKSLAEIRIHENKVKIKQDFTKGM 193
Db 72 NAGI-----PSDLKLLKVERIYIYNSLDEFPNLPKYVKELHQLQENNIRITITDLSKI 127

QY 194 NALHVLMSANPLDNNNGIEPGAFEGVTVFHIR-IAEAKLTSVPKGLPPTLLELHLDYNKI 252
Db 128 PYLEELHLDNNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRI 187

QY 253 STVELEDFRYKELORLGLGNKKTIDENG--LANIPRVREIHLNENKLLKIPSGLP 310
Db 188 STISSPSLQGLTSLKRLVLDGNLNNHGLGDKVFFNLVNLTELSLRNSLTAAPVNLPGT 247

QY 311 KYLQIIFLHSNSIARVGNDF 331
Db 248 N-LRKLYLQDNHINRVPNPF 267
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; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 132
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-616-132

Query Match 16.6%; Score 331.5; DB 9; Length 649;
Best Local Similarity 33.0%; Pred. No. 4.1e-20;
Matches 86; Conservative 37; Mismatches 111; Indels 27; Gaps 5;

QY 74 CPFGCQCYRVVHCSDLGTSVPTNPFDTRMLDLQNNKKEIKENDFKGLTSLYGLILN 133
DB 31 CPSCVRCDCAGFIYCNDRFLTSIPTGIPEDATTLYLQNNQI-----N 71

QY 134 NKKLTKEHPKAFLETTKKLRRLYLHSHNOLSEIPLNPKSLAELRIHENKVKKIQKDTFKGM 193
DB 72 NAGI-----PSDLKLLKVERIYLYHNSLDEFTNLPKVKVKEHLQENNRITTYDSLKI 127

QY 194 NALHVLMSANPLDNNNGIEPCAFEGVTVFHIR-IAEAKLTSVPKGLPPTLLEHLHDYDKI 252
DB 128 PYLEELHLDNDSVSAVSIEEGAFRDSNYLRLFLSRNHLSTIPWGLPRTIEELRLDDNRI 187

QY 253 STVELEDFKRYKELQRLGLGNKKTIDTENG--LANIPRVREIHLNENKLLKIPSGLP 310
DB 188 STISSPSLQGLTSLKRLVLDGNLLNHHGLGDKVFFNLVNLTELSLRNSLTAAPVNLPGT 247

QY 311 KYLOIFLHNSIARVGVNDF 331
DB 248 N-LRKLQLQDNHINRVPNAP 267

RESULT 31
US-10-006-867-132
; Sequence 132, Application US/10006867
; Patent No. US20020119130A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/006,867
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/063435
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/064215
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089952

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;	PRIOR FILING DATE:	1998-06-19
;	PRIOR APPLICATION NUMBER:	60/090246
;	PRIOR FILING DATE:	1998-06-22
;	PRIOR APPLICATION NUMBER:	60/090444
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090688
;	PRIOR FILING DATE:	1998-06-25
;	PRIOR APPLICATION NUMBER:	60/090696
;	PRIOR FILING DATE:	1998-06-25
;	PRIOR APPLICATION NUMBER:	60/090862
;	PRIOR FILING DATE:	1998-06-26
;	PRIOR APPLICATION NUMBER:	60/091628
;	PRIOR FILING DATE:	1998-07-02
;	PRIOR APPLICATION NUMBER:	60/096012
;	PRIOR FILING DATE:	1998-08-10
;	PRIOR APPLICATION NUMBER:	60/096757
;	PRIOR FILING DATE:	1998-08-17
;	PRIOR APPLICATION NUMBER:	60/096949
;	PRIOR FILING DATE:	1998-08-18
;	PRIOR APPLICATION NUMBER:	60/096959
;	PRIOR FILING DATE:	1998-08-18
;	PRIOR APPLICATION NUMBER:	60/097954
;	PRIOR FILING DATE:	1998-08-26
;	PRIOR APPLICATION NUMBER:	60/097971
;	PRIOR FILING DATE:	1998-08-26
;	PRIOR APPLICATION NUMBER:	60/097979
;	PRIOR FILING DATE:	1998-08-26
;	PRIOR APPLICATION NUMBER:	60/098749
;	PRIOR FILING DATE:	1998-09-01
;	PRIOR APPLICATION NUMBER:	60/099741
;	PRIOR FILING DATE:	1998-09-10
;	PRIOR APPLICATION NUMBER:	60/099763
;	PRIOR FILING DATE:	1998-09-10
;	PRIOR APPLICATION NUMBER:	60/099792
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;	PRIOR APPLICATION NUMBER:	60/099812
;	PRIOR FILING DATE:	1998-09-10
;	PRIOR APPLICATION NUMBER:	60/099815
;	PRIOR FILING DATE:	1998-09-10
;	PRIOR APPLICATION NUMBER:	60/100627
;	PRIOR FILING DATE:	1998-09-16
;	PRIOR APPLICATION NUMBER:	60/100662
;	PRIOR FILING DATE:	1998-09-16
;	PRIOR APPLICATION NUMBER:	60/100683
;	PRIOR FILING DATE:	1998-09-17
;	PRIOR APPLICATION NUMBER:	60/100684
;	PRIOR FILING DATE:	1998-09-17
;	PRIOR APPLICATION NUMBER:	60/100930
;	PRIOR FILING DATE:	1998-09-17
;	PRIOR APPLICATION NUMBER:	60/101279
;	PRIOR FILING DATE:	1998-09-22
;	PRIOR APPLICATION NUMBER:	60/101475
;	PRIOR FILING DATE:	1998-09-23
;	PRIOR APPLICATION NUMBER:	60/101738
;	PRIOR FILING DATE:	1998-09-24
;	PRIOR APPLICATION NUMBER:	60/101743
;	PRIOR FILING DATE:	1998-09-24
;	PRIOR APPLICATION NUMBER:	60/101916
;	PRIOR FILING DATE:	1998-09-24
;	PRIOR APPLICATION NUMBER:	60/102570
;	PRIOR FILING DATE:	1998-09-30
;	PRIOR APPLICATION NUMBER:	60/103449
;	PRIOR FILING DATE:	1998-10-06
;	PRIOR APPLICATION NUMBER:	60/103678
;	PRIOR FILING DATE:	1998-10-08
;	PRIOR APPLICATION NUMBER:	60/103679
;	PRIOR FILING DATE:	1998-10-08
;	PRIOR APPLICATION NUMBER:	60/103711
;	PRIOR FILING DATE:	1998-10-08
;	PRIOR APPLICATION NUMBER:	60/105000
;	PRIOR FILING DATE:	1998-10-20
;	PRIOR APPLICATION NUMBER:	60/105002
;	PRIOR FILING DATE:	1998-10-20

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 ; PRIOR APPLICATION NUMBER: 60/089908
 Query Match 16.6%; Score 331.5; DB 12; Length 649;
 Best Local Similarity 33.0%; Pred. No. 4.le-20;
 Matches 86; Conservative 37; Mismatches 111; Indels 27; Gaps 5;
 QY 74 CPEGCCQYSRVHVHCDLGLTSVPTNIPEDTRMLDQNNKIKEIKENDFKGLTSLYGLILN 133
 DB 31 CFSVCKDAGFYICNDRLFTSIPTGIPEDATLYLQNNQI-----N 71
 QY 134 NNKLTAKIHPKAFLTTKLRLRYLSHNSQLSEIPLNLPKSLAELRIHENKVKXIOKDTFGM 193
 DB 72 NAGI---PSDLKNLLKVERIYLYHNSLDEPPTNLPKYVKELHLQENNIPTVDSLSKI 127
 QY 194 NALHVLMSANPLDNNGIEPGAFEGVTVFHIR-TAEAKLTSVPKGLPPTLLELHLDYANKI 252
 DB 128 PYLEELHLDNDSVSAVSIEBGAFRDSNYLRLLFUSRNHLSTIPWGLPRTIBELRLDDNRI 187
 QY 253 STVELEDFKRYKELQRLGLGNKKTIDENG--LANIPRVREIHLNENKKKIPSGLP 310
 DB 188 STISSPSLQGLTSLKRLVLDGNLNNHGLGDKVFFENLVNLTLSLVRSNLTAAAPVNLPGT 247
 QY 311 KYLOIFLHNSIARVGNDF 331
 DB 248 N-LRKLYLQDNHINRVPNPF 267

RESULT 33
 US-10-028-072-370
 ; Sequence 370, Application US/10028072
 ; Publication No. US20030004311A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: Deforge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tamas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang
 ; TITLE OF INVENTION:
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/028,072
 ; CURRENT FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 60/049911
 ; PRIOR FILING DATE: 1997-06-18
 ; PRIOR APPLICATION NUMBER: 60/056974
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52	PRIOR APPLICATION NUMBER: 60/086414
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58	PRIOR APPLICATION NUMBER: 60/088026
59	PRIOR FILING DATE: 1998-06-04
60	PRIOR APPLICATION NUMBER: 60/088730
61	PRIOR FILING DATE: 1998-06-10
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70	PRIOR APPLICATION NUMBER: 60/089599
71	PRIOR FILING DATE: 1998-06-17
72	PRIOR APPLICATION NUMBER: 60/089907
73	PRIOR FILING DATE: 1998-06-18

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; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

Query Match      16.5%; Score 329; DB 9; Length 642;
Best Local Similarity 29.1%; Pred. No. 6.6e-20;
Matches 98; Conservative 55; Mismatches 146; Indels 38; Gaps 9;

QY 51 EDNSLFTPTREPSHFPPDLP-----MCPFGCQCYSR-VHCSDLGLTSVPTNIPDTR 104
DB 70 EENE-FAEEEPVVLSPPEPGPAAVSCPRDCACSOEGVVDGGIDLREFPGDLPEHTN 128
QY 105 MLDLQNNKIKIKENDFKGLTSYGLTLNKNKLT--IHPKATLTTKRLRLYSHNOLS 162
DB 129 HLSLQNNQLEKIYPEELSRHLRLETLNQNRLTSRGLPEKAHEHTLNLYLANNKLT 188
QY 163 EIPNLKPSLAELRIHENKVKKIOKDTFGMNAHVLMSANPLDNNNGIEPGAFEGVTVF 222
DB 189 LAPRLFNALISVDFAANYLTLYGLTFGQKPNLRSVYLHNNKLADAGLDDNMFNGSSNV 248
QY 223 HIRTAER-LTSVPKGLPPLLEHLHDYNKISTVELEDFRKYRELQRLGNNKKTID--I 279
DB 249 EVLILSSNLRHVPHKLPALYKLIHLKNNKLEKIPPGAFSELSSRLYLNQNYLTDEGL 308
QY 280 ENGLANIPRVRETHLENNKIKIPSGLPE-----LKYLIQIIF 317
DB 309 DNETFWKLSLEYLDLSNNLSRVPAGLPRSLVLLHLEKNAIRSVANVLTPIRSLEYLL 368
QY 318 LHSNSIARVGVDNCPPTVPKMKKSLYSALSLFNPNVK 354
DB 369 LHSNQLREQGIH---PLAFGLKRLHT-VHLYNNALE 401

RESULT 34
US-09-925-301-1192
; Sequence 1192, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1192
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (11)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE

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; LOCATION: (13)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1192

Query Match      16.2%; Score 323; DB 10; Length 415;
Best Local Similarity 26.4%; Pred. No. 1.2e-19;
Matches 87; Conservative 64; Mismatches 131; Indels 48; Gaps 9;

QY 63 SHEFPDLPFM-----CPFGCOC---YSRVVHCSDLG 91
DB 76 TYIDYDYPYETYPYPYGVDEGPAYTYGSPSPDPDCEQCPNFTAMTCNARN 135
QY 92 LTSVPTNIPDTRMLDLQNNKIKIKENDFKGLTSYGLTLNKNKLT--KIHPKAFLTTK 149
DB 136 LAYLPP-VPSRMKYVYFQNNQITSIOEGVDNATGLLWALHNGOITSDKVGKRVFSKLR 194
QY 150 KLRRLYSHNQLSEIPLNLPKSLAEIRIHNKVKKIOKDTFGMNAHVLMSANPLDNN 209
DB 195 HLERLYLDHNNLTRMPGLPRSLREHLHDHNOISRPVNNALEGLNLTALYLOHNEIOEV 254
QY 210 GIEPGAFEGV-TVFHIRTAERAKLTVPKGLPPTLLEHLHDYNKISTVELEDFKRYKELOR 268
DB 255 G---SSMGLRSLIILDLSYNHLRKPVDGLPSALEQLWMEHNNVTVPDSYTRGAPKLLY 311
QY 269 LGLGNKKTIDENGSLA-----NIPRVRETHLENNKIKIPSGLPKLYLIQIFLHSNSIA 324
DB 312 VRLSHNSLT---NNGLASNTFNSSSLELDELDSYNQLQKIP---PVNTNLENLYLQGNRIN 365
QY 325 RVGVNDFCPTVPKMKKSLYSALSLFNPNVK 354
DB 366 EFSISFCTVVDVNVFSLQVLRDLGNEIK 395

RESULT 35
US-09-905-201A-28
; Sequence 28, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US/09/905,291A
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
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; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698

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; PRIOR FILING DATE: 1999-07-26
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; PRIOR FILING DATE: 1999-09-13
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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 28
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-291A-28

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Query Match      15.7%; Score 313.5; DB 9; Length 660;
Best Local Similarity 27.7%; Pred. No. 1.4e-18;
Matches 79; Conservative 62; Mismatches 109; Indels 35; Gaps 8;

QY 74 CPFGCQYRVVHCSDLGTSVPTNIPDTRMLDQNNKKEIKENDFKGLTSLYGLILN 133
Db 36 CPSCRCRDRNFVYCNERSLTSVPLGIP-----EGVTVLY---LH 71

QY 134 NKLTKI-HPKAFLLTKRLRLYLHSHNOLSEIPLNPKSLAELRIHENKVKIKOKDFKG 192
Db 72 NNQINNAGFPAELHNVQSVHTVLYGNQDDEFPMNLKPNVRLHLQENNQTISRALAQ 131

QY 193 MNALHVLSEMSANPLDNGNIEGAF-EGVTVPFHRIAEAKLTSPKGLPPTLLEHLHDYNK 251
Db 132 LKLEELHLDNDSISTGVGEDGAFREATISLKLFLSKNHLSSVPVGLPVDQLQELRVDENR 191

QY 252 ISTVELEDFKRYKELORGLGNKKTID--IENGSIANIPRVRETHLENNKIKKTPSGIPE 309
Db 192 IAVISDMAFQNLTSUERIVDGNLTLNKGTAEGFTSHLTKLKEFSIVRNSLSLHPPDLP 251

QY 310 LKYLIQIFLHNSIARVGNDPCTVPKMKKSLYSALSIFNNPVK 354
Db 252 THLIR-LYLDQNIQHIIPLTAF-SNLKRLER-----LDISNNQLR 289

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RESULT 36
US-10-066-500-115
; Sequence 115, Application US/10066500
; Patent No. US20020177165A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Bolstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong

```

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; APPLICANT: Wei-Oiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Geritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130R1C7
; CURRENT APPLICATION NUMBER: US/10/066,500
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24

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; PRIOR APPLICATION NUMBER: 60/106032
; PRIOR FILING DATE: 1998-10-28
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; PRIOR APPLICATION NUMBER: 09/548815
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; PRIOR APPLICATION NUMBER: 09/664610
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; PRIOR FILING DATE: 2000-09-18
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; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 09/802706
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; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 15.7%; Score 313.5; DB 9; Length 660;

Best Local Similarity 27.7%; Pred No. 1.4e-18;

Matches 79; Conservative 62; Mismatches 109; Indels 35; Gaps 8;

QY 74 CPGCQCYSRVVHCSDLGTSVPTNIPDTRMLDLQNNKIKIKENDFKGLTSLYGLILN 133

DB 36 CFSVCRCDRNFVVCNERSLTSVPLGIP-----EGVTVLY---LH 71

QY 134 NNKLTKI-HPKAFITTKLRRLYLSHNQSLSEIPLNPKSLAELRIHENKVKKIQKDTFG 192

DB 72 NNQINNAGFPALHNVSHTVLYGNQLDEFPMLPNKRVRLHLENNIQTISRALLAQ 131

QY 193 MNALHVLEMSANPLDNNNGTEPGAF-EGVTVFHRTIAEAKLTSPKGLPPTLLELHDYNK 251

DB 132 LKLELHLDNDSISITGVGEDGAFREAIKLLFLSKNHLSSVPVGLPVDLQELRVENR 191

QY 252 ISTVELEDFKRYKEIQRGLGNKKTID--IENGSLANIPRVREIHLENNKLIKPSGLPE 309

DB 192 IAVISDMAFQNTLSERLIYDGNLLTNKGIAGTFSHTLTKKEFSIVRNSLSHPPDLPFG 251

QY 310 LKYLOIIFLHSNSIARVGVNDFCPTVPKMKSLYSALSIFNNPVK 354

DB 252 THLIR-LYLQDQNIHIPTAF-SNURKLER-----LDSNNQLR 289

RESULT 37

US-09-902-853-28

; Sequence 28, Application US/09902853

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; Publication No. US200020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
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; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 28
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-902-853-28

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Query Match 15.7%; Score 313.5; DB 9; Length 660;
Best Local Similarity 27.7%; Pred. No. 1.4e-18;
Matches 79; Conservative 62; Mismatches 109; Indels 35; Gaps 8;

QY 74 CPFGCCQCYRVHVCSDIGLTSVPTNIPFDTRMLDLQNNKIKEKDNDFKGLTSLYGLILN 133
   || || || || || || || || || || || || || || || || || || || || ||
Db 36 CPVSCRCDRNFVVCNERSLTSVPLGIP-----EGVTVLY---LH 71
   || || || || || || || || || || || || || || || || || || || || ||

QY 134 NNKLTKI-HPKAEFLTYYKRLRLYLSHNSQLSEIPLNPKSLAEIRIHENKVKIKQDTFKG 192
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Db 72 NNQINNAGFPAELHNVOSVHTVLYQNLDEFPNPLPKVNVRLHLOENNIQTSRAALAQ 131
   || || || || || || || || || || || || || || || || || || || || ||

QY 193 MNALHVLMSANPLDNNNGIEPGAF-EGVTVEFHIRIAEAKLTSPKGLPPTLLELHLDYNK 251
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 132 LLKLEELHDDNSISIVGVEDGAFRAISLKLFLSKNLSVPGVGLVDQLERVDENR 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 252 ISTVELEDFKRYKELQRLGLGNKKTID--TENGSLANIPRVREIHLNKKKKIPSGLPE 309
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 192 IAVISDMAFQNLTSLERLIVDGNLLTKGTAEGTFSHLTKLKEFSIVRNSLSHPPDPLPG 251
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 310 LKYLQIIFLHSNSIARVGNDFCPTVPKMKKSLYSALSIFLNNPVK 354
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 252 THLIR-LYLODNQINHIPLTAF-SNLRKLER-----LDISNNQLR 289
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RESULT 38
US-09-907-824-28
; Sequence 28, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944

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APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,841
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
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PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 28
LENGTH: 660
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-824-28

Query Match 15.7%; Score 313.5; DB 9; Length 660;
Best Local Similarity 27.7%; Pred. No. 1.4e-18;
Matches 79; Conservative 62; Mismatches 109; Indels 35; Gaps 8;
Qy 74 CPFGCOCYRVVHCSDLGTSVPTNIPDTRMLDLQNNKIKEIKENDFKGLTSYGLILN 133
Db 36 CPSVCRDRNFVYCNERSLTSVPLGIP-----EGVTVLV---LH 71
Qy 134 NKLTKI-HPKAFITTKRLRLYLSHNQLSEIPLNPKSLAEIRIHENKVKIKQKDTFG 192
Db 72 NNQINNAGFPAELHNVQSVHTVLYGNQLDEFPNLPKNRVVLHQLQNNIQTISRALAQ 131
Qy 193 MNALHVLMSANPLDNGIEPGAF-EGVTVFHRIAEAKLTSPKGLPTLLELHLDYNK 251
Db 132 LKLEELHLDNNSITFVGVEDGAFREAIKLLFLSKNHLSSVPVGLPVDQLRLVDENR 191
Qy 252 ISTVELEDFKRYKELQRLGLGNKKTID--IENGSLANIPRVREIHLENNKLLKIPSGLE 309
Db 192 IAVISDMAFQNLTSERLIVDGNLLTNKGAEGTFSHLTKLKEFSIVRNSLSHPPDPLG 251
Qy 310 LKYLQIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSIFNNPVK 354
Db 252 THLIR-LYLODQNIHPLTAF-SNLRKLER-----LDISNNQLR 289

RESULT 39
US-09-907-841-28
Sequence 28, Application US/09907841
Publication No. US20020198366A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,841
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
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PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 28
LENGTH: 660
TYPE: PRT
ORGANISM: Homo sapiens
US-09-907-841-28

Query Match 15.7%; Score 313.5; DB 9; Length 660;
Best Local Similarity 27.7%; Pred. No. 1.4e-18;
Matches 79; Conservative 62; Mismatches 109; Indels 35; Gaps 8;
Qy 74 CPFGCOCYRVVHCSDLGTSVPTNIPDTRMLDLQNNKIKEIKENDFKGLTSYGLILN 133
Db 36 CPSVCRDRNFVYCNERSLTSVPLGIP-----EGVTVLV---LH 71
Qy 134 NKLTKI-HPKAFITTKRLRLYLSHNQLSEIPLNPKSLAEIRIHENKVKIKQKDTFG 192
Db 72 NNQINNAGFPAELHNVQSVHTVLYGNQLDEFPNLPKNRVVLHQLQNNIQTISRALAQ 131
Qy 193 MNALHVLMSANPLDNGIEPGAF-EGVTVFHRIAEAKLTSPKGLPTLLELHLDYNK 251
Db 132 LKLEELHLDNNSITFVGVEDGAFREAIKLLFLSKNHLSSVPVGLPVDQLRLVDENR 191
Qy 252 ISTVELEDFKRYKELQRLGLGNKKTID--IENGSLANIPRVREIHLENNKLLKIPSGLE 309
Db 192 IAVISDMAFQNLTSERLIVDGNLLTNKGAEGTFSHLTKLKEFSIVRNSLSHPPDPLG 251
Qy 310 LKYLQIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSIFNNPVK 354
Db 252 THLIR-LYLODQNIHPLTAF-SNLRKLER-----LDISNNQLR 289

RESULT 40
US-09-904-011-28
Sequence 28, Application US/09904011

Publication No. US20030003530A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,011
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 28
LENGTH: 660
TYPE: PRT
ORGANISM: Homo Sapien

US-09-904-011-28

Query Match 15.7%; Score 313.5; DB 9; Length 660;
Best Local Similarity 27.7%; Pred. No. 1.4e-18;
Matches 79; Conservative 62; Mismatches 109; Indels 35; Gaps 8;
QY 74 CPFGCOCYSRVVHCSDGLGTSVPTNIPFDTRMLDLQNNKIKEKENDFKGLTSLYGLIILN 133
Db 36 CPSVCRCDNFVYCNSRSLSVPLGIP-----EGVTVLY---LH 71
QY 134 NNKLTKI-HPKAFLLTKKLRRLYLHSHNQLSEIPLNLPKSLAEIRIHENKVKIKQDKTFKG 192
Db 72 NNQINNAGPFAELHNVQSVHTVLYGNQLDEPMMNLPKNVRVLHLQENNIQIISRAALAQ 131
QY 193 MNALHVLMSANPLDNNGIEPGAF-EGVTVFHIRIAEAKLTSPKGLPPTLLELHLDYKN 251
Db 132 LLKLEELHLDNDSISTVGVEDGAFREAISLKLFLSKNHLSSVPGVLDLQELRYDENR 191
QY 252 ISTVELEDFKRYKELQRLGLGNKKITD--IENGSLANIPRVREIHLNKKIKIPSGLPE 309
Db 192 IAVISDMATQNTLSLERLIVDGNLNTKGLAEGTFSHLTKLKFEFSIVRNSLSHPPDPLPG 251
QY 310 LKYLQIIFLHNSIARVGVNDFCTVPVKMKKSLYSIAISLFNNPVK 354
Db 252 THLIR-LYLQDNQINHIPLTAF-SNLKLER-----LDISNNQLR 289

RESULT 41

US-10-028-072-350
Sequence 350, Application US/10028072
Publication No. US20030004311A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19

,	PRIOR FILING DATE:	1998-03-25
,	PRIOR APPLICATION NUMBER:	60/0796663
,	PRIOR FILING DATE:	1998-02-27
,	PRIOR APPLICATION NUMBER:	60/079728
,	PRIOR FILING DATE:	1998-03-27
,	PRIOR APPLICATION NUMBER:	60/080165
,	PRIOR FILING DATE:	1998-03-31
,	PRIOR APPLICATION NUMBER:	60/081203
,	PRIOR FILING DATE:	1998-04-09
,	PRIOR APPLICATION NUMBER:	60/081229
,	PRIOR FILING DATE:	1998-04-09
,	PRIOR APPLICATION NUMBER:	60/081695
,	PRIOR FILING DATE:	1998-04-14
,	PRIOR APPLICATION NUMBER:	60/081817
,	PRIOR FILING DATE:	1998-04-15
,	PRIOR APPLICATION NUMBER:	60/081918
,	PRIOR FILING DATE:	1998-04-15
,	PRIOR APPLICATION NUMBER:	60/082999
,	PRIOR FILING DATE:	1998-04-24
,	PRIOR APPLICATION NUMBER:	60/083322
,	PRIOR FILING DATE:	1998-04-28
,	PRIOR APPLICATION NUMBER:	60/083545
,	PRIOR FILING DATE:	1998-04-29
,	PRIOR APPLICATION NUMBER:	60/084600
,	PRIOR FILING DATE:	1998-05-07
,	PRIOR APPLICATION NUMBER:	60/084627
,	PRIOR FILING DATE:	1998-05-07
,	PRIOR APPLICATION NUMBER:	60/084637
,	PRIOR FILING DATE:	1998-05-07
,	PRIOR APPLICATION NUMBER:	60/085149
,	PRIOR FILING DATE:	1998-05-12
,	PRIOR APPLICATION NUMBER:	60/085323
,	PRIOR FILING DATE:	1998-05-13
,	PRIOR APPLICATION NUMBER:	60/085338
,	PRIOR FILING DATE:	1998-05-13
,	PRIOR APPLICATION NUMBER:	60/085339
,	PRIOR FILING DATE:	1998-05-13
,	PRIOR APPLICATION NUMBER:	60/085579
,	PRIOR FILING DATE:	1998-05-15
,	PRIOR APPLICATION NUMBER:	60/085697
,	PRIOR FILING DATE:	1998-05-15
,	PRIOR APPLICATION NUMBER:	60/085704
,	PRIOR FILING DATE:	1998-05-15
,	PRIOR APPLICATION NUMBER:	60/086414
,	PRIOR FILING DATE:	1998-05-22
,	PRIOR APPLICATION NUMBER:	60/086430
,	PRIOR FILING DATE:	1998-05-22
,	PRIOR APPLICATION NUMBER:	60/087106
,	PRIOR FILING DATE:	1998-05-28
,	PRIOR APPLICATION NUMBER:	60/088026
,	PRIOR FILING DATE:	1998-06-04
,	PRIOR APPLICATION NUMBER:	60/088730
,	PRIOR FILING DATE:	1998-06-10
,	PRIOR APPLICATION NUMBER:	60/088741
,	PRIOR FILING DATE:	1998-06-10
,	PRIOR APPLICATION NUMBER:	60/088810
,	PRIOR FILING DATE:	1998-06-10
,	PRIOR APPLICATION NUMBER:	60/088958
,	PRIOR FILING DATE:	19/98-06-11
,	PRIOR APPLICATION NUMBER:	60/089532
,	PRIOR FILING DATE:	1998-06-17
,	PRIOR APPLICATION NUMBER:	60/089599
,	PRIOR FILING DATE:	1998-06-17
,	PRIOR APPLICATION NUMBER:	60/089907
,	PRIOR FILING DATE:	1998-06-18
,	PRIOR APPLICATION NUMBER:	60/089947
,	PRIOR FILING DATE:	1998-06-19
,	PRIOR APPLICATION NUMBER:	60/090349
,	PRIOR FILING DATE:	1998-06-23
,	PRIOR APPLICATION NUMBER:	60/090429
,	PRIOR FILING DATE:	1998-06-24
,	PRIOR APPLICATION NUMBER:	60/090445
,	PRIOR FILING DATE:	1998-06-24

; PRIOR APPLICATION NUMBER: 60/090538
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090863
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/091360
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091519
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07

Query Match 15.7%; Score 313.5; DB 9; Length 660;
 Best Local Similarity 27.7%; Pred. No. 1.4e-18;
 Matches 79; Conservative 62; Mismatches 109; Indels 35; Gaps 8;

QY 74 CPFGCCYSRVHCSDGLTSTVPTNIPEDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
 Db 36 CPVCRDRNFVYCNERSLTSVPLGIP-----EGVTVLY---LH 71
 QY 134 NKKLTKI-HPKAFLTTKLRLLSHNOLSEIPLNPKSLAEIRHENKVKKIQKDTFG 192
 Db 72 NNQINNAGFAELHNVQSVHTVLYGNLDDEFFMNLPRNVRVHLHQENNIQTISRALAQ 131
 QY 193 MNALHVLEMSANPLDNNNGIEGAF-EGVTVFHIRIAEAKLTSPKGLPPTLLEHLHDYNK 251
 Db 132 LLKLEELHLDNDSISTVGVEDGAFREAIKLLFLSKNHLSSVPVGLPVDLQELRVDENR 191
 QY 252 ISTVELEDFKRYKELQRLGLGNKTTD--IENGSLANTPRVREIHLNKKLKIPSGLPE 309
 Db 192 IAVISDMAFQNLTSERLIVDGNLTNKGIAEGTFSHTTKLKEFSIVRNSLSLHPPDPLPG 251
 QY 310 LKYLQIIFLHNSIARVGVDNFCPTVPKMKKSLYSALSIFNNPVK 354
 Db 252 THLIR-LYLDQNOINHPIPTAF-SNLRKLER-----LDISNNQLR 289

RESULT 42

US-09-909-320-28
 ; Sequence 28, Application US/09909320
 ; Patent No. US20020132240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Klijavin, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/909,320
 ; CURRENT FILING DATE: 2002-01-04
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 60/146,222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594
 ; PRIOR FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944
 ; PRIOR FILING DATE: 1999-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219
 ; PRIOR FILING DATE: 2000-01-05
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 28
 ; LENGTH: 660
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-909-320-28

Query Match 15.7%; Score 313.5; DB 10; Length 660;
 Best Local Similarity 27.7%; Pred. No. 1.4e-18;
 Matches 79; Conservative 62; Mismatches 109; Indels 35; Gaps 8;

QY 74 CPFGCCYSRVHCSDGLTSTVPTNIPEDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
 Db 36 CPVCRDRNFVYCNERSLTSVPLGIP-----EGVTVLY---LH 71
 QY 134 NKKLTKI-HPKAFLTTKLRLLSHNOLSEIPLNPKSLAEIRHENKVKKIQKDTFG 192
 Db 72 NNQINNAGFAELHNVQSVHTVLYGNLDDEFFMNLPRNVRVHLHQENNIQTISRALAQ 131
 QY 193 MNALHVLEMSANPLDNNNGIEGAF-EGVTVFHIRIAEAKLTSPKGLPPTLLEHLHDYNK 251
 Db 132 LLKLEELHLDNDSISTVGVEDGAFREAIKLLFLSKNHLSSVPVGLPVDLQELRVDENR 191
 QY 252 ISTVELEDFKRYKELQRLGLGNKTTD--IENGSLANTPRVREIHLNKKLKIPSGLPE 309
 Db 192 IAVISDMAFQNLTSERLIVDGNLTNKGIAEGTFSHTTKLKEFSIVRNSLSLHPPDPLPG 251
 QY 310 LKYLQIIFLHNSIARVGVDNFCPTVPKMKKSLYSALSIFNNPVK 354
 Db 252 THLIR-LYLDQNOINHPIPTAF-SNLRKLER-----LDISNNQLR 289

RESULT 43

US-09-909-088B-28
 ; Sequence 28, Application US/09909088B
 ; Patent No. US20020146709A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc

Db 421 SLSLYDNNIQ--SLANGTFDAMKSMKTVHL 449

RESULT 45

US-10-174-590-290

; Sequence 290, Application US/10174590

; Publication No. US20030008352A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430RIC42

; CURRENT APPLICATION NUMBER: US/10/174,590

; CURRENT FILING DATE: 2002-06-18

; Prior application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 290

; LENGTH: 1523

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-174-590-290

Query Match

Best Local Similarity 15.5%; Score 309; DB 9; Length 1523;

Matches 98; Conservative 58; Mismatches 114; Indels 124; Gaps 9;

QY 74 CPFGCCYSRVVHCSDGLTSVPTNPFDTRMLDQNNKIKEIKENDFKGLTSLYGLILN 133

Db 34 CPTKCTCSAASVDCGGLRAVPRGIPRPAERLDRNNITRTYKMFAGLKNLRVHL 93

QY 134 NNKLTKIHPKAFLTTKRLRLYLSHNQLSEIPLNPKS---LAELRIHENKVKKIOKDTF 190

Db 94 DNOVSIVIERGAFQDLKQLERLRNKNKQLVPELLFQSTPKLRDLSENQIQIPKAF 153

QY 191 KGMNALHVLMSANPLDNG---TEPGAFEG-----VTVF----- 222

Db 154 RGITDVKNLQ-----LDNNHISCIEDGAFRALRDLLEITLNNNISRLVTSFNHMPKIR 208

QY 223 -----HIR---IAEAK----- 230

Db 209 TLRHLSNHLCDCHLAWLSDMLRQRTVGOFTLCMAPVHLRGFNADVOKKEYVCPAPHS 268

QY 231 -----LTSVPKGLPPTLLEHLDYNNKISTVELEDFK 261

Db 269 EPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIVEIRLEQNSIKAIPAGFT 328

QY 262 RYKELQRLGLGNKKTIDTENGSLANIPRVREIHLNKNLKKIPSGLPE-LKYLIQIPLHS 320

Db 329 QYKKLRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAKGLFDGLVSLQLLLNA 388

QY 321 NSIARGVNDFCPTVPKMKKSLYSALSIFNNPVK 354

Db 389 NKINCLRVNTF-----QDLQNLNLLSLYDNKLQ 416

RESULT 46

US-10-176-758-290

; Sequence 290, Application US/10176758

; Publication No. US20030008353A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 290
; LENGTH: 1523
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-758-290

Query Match 15.5%; Score 309; DB 9; Length 1523;

Best Local Similarity 24.9%; Pred. No. 9.6e-18;

Matches 98; Conservative 58; Mismatches 114; Indels 124; Gaps 9;

QY 74 CPFGCCYSRVVHCSDGLTSVPTNPFDTRMLDQNNKIKEIKENDFKGLTSLYGLILN 133

Db 34 CPTKCTCSAASVDCGGLRAVPRGIPRPAERLDRNNITRTYKMFAGLKNLRVHL 93

QY 134 NNKLTKIHPKAFLTTKRLRLYLSHNQLSEIPLNPKS---LAELRIHENKVKKIOKDTF 190

Db 94 DNOVSIVIERGAFQDLKQLERLRNKNKQLVPELLFQSTPKLRDLSENQIQIPKAF 153

QY 191 KGMNALHVLMSANPLDNG---IEPGAFEG-----VTVF----- 222

Db 154 RGITDVKNLQ-----LDNNHISCIEDGAFRALRDLLEITLNNNISRLVTSFNHMPKIR 208

QY 223 -----HIR---IAEAK----- 230

Db 209 TLRHLSNHLCDCHLAWLSDMLRQRTVGOFTLCMAPVHLRGFNADVOKKEYVCPAPHS 268

QY 231 -----LTSVPKGLPPTLLEHLDYNNKISTVELEDFK 261

Db 269 EPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIVEIRLEQNSIKAIPAGFT 328

QY 262 RYKELQRLGLGNKKTIDTENGSLANIPRVREIHLNKNLKKIPSGLPE-LKYLIQIPLHS 320

Db 329 QYKKLRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAKGLFDGLVSLQLLLNA 388

QY 321 NSIARGVNDFCPTVPKMKKSLYSALSIFNNPVK 354

Db 389 NKINCLRVNTF-----QDLQNLNLLSLYDNKLQ 416

RESULT 47

US-10-175-737-290

; Sequence 290, Application US/10175737

; Publication No. US20030013153A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430RIC50

[illegible]

; PRIOR FILING DATE: 1998-06-16
 ; PRIOR APPLICATION NUMBER: 60/089514
 ; PRIOR FILING DATE: 1998-06-16
 ; PRIOR APPLICATION NUMBER: 60/089538
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089598
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089653
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089908

Query Match 15.5%; Score 309; DB 12; Length 1523;
 Best Local Similarity 24.9%; Pred. No. 9.6e-18;
 Matches 98; Conservative 58; Mismatches 114; Indels 124; Gaps 9;

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QY 74 CPFGCQCYSRVHCSDLGLTSVPTNIPEDTRMLDQNNKKEIKENDFKGLTSLYGLILN 133
Db 34 CPTKCTSAASVDCGHLGLRAVRPGIPRPAERDLDRNTRITKMDFAGLKNLRVLHLE 93
QY 134 NNKLTKIHPKAFLTTKLRRLYLSHNOLSEIPLNPKS----LAELRIHENKVKKIQKDTF 190
Db 94 DNQSVTIERGAFQDLKLERLRNKNKLOVLPELLFQSTPKLTRLDLSENIQIOPRKAF 153
QY 191 KGMALHVLMSANPLDNG---IEPCAFEG-----VTVF----- 222
Db 154 RGITDVKNLQ-----LDNNHITSIEDGAFRALRDLEILTLLNNNNISRLVTSFNHMPKIR 208
QY 223 -----HIR-----IAEAK----- 230
Db 209 TRLHSHLYCDCHLWLDLQRRTVQGTLCMAPVHLRGFNADVQKKEYVCAPHS 268
QY 231 -----LTSVPKGLPPTLLEHLHDYNNKISTVELEDFK 261
Db 269 EPPSCNANSISCPSPCTCSNNIVDCRGKGLMETPANLPEGIVEIRLEQNSIKAIPAGAF 328
QY 262 RYKELQRLGLGNKKTIDENGSLANIPRVREIHLNENKLNKIPSGLPK-LKYLIQIIFLHS 320
Db 329 QYKRLRIDISKNGIDISADAFGLKSLTSLVLYGNKITEIAKGLFDGLVSLQLLLLNA 388
QY 321 NSIARVGVNDPCTVPKMKKSLXSALSIFNNPVK 354
Db 389 NKINCLRVNTF-----QDLQNLNLLSLYDNKLQ 416
  
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RESULT 50

US-10-063-547-124
 ; Sequence 124, Application US/10063547
 ; Publication No. US20020182638A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan J.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,547
 ; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 124
 ; LENGTH: 513
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-063-547-124

Query Match 15.3%; Score 304.5; DB 9; Length 513;
 Best Local Similarity 28.8%; Pred. No. 5.5e-18;

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Matches 87; Conservative 57; Mismatches 105; Indels 53; Gaps 9;
QY 74 CPFGCQCYSRVHCSDLGLTSVPTNIPEDTRMLDQNNKKEIKENDFKGLTSLYGLILN 133
Db 34 CPKGCRCCKWYCYCSQKLOETIPSSISAGCLGLSLRYNSLOKLYNQKGLNQLTWLYLD 93
QY 134 NNKLTKIHPKAFLTTKLRRLYLSHNOLSEIPLNPKSLAELRIHENKVKKIQKDTFKGM 193
Db 94 HNHISNIDENAFNGIRRLKELILSSNRISYF-LN-----NTERPV 132
QY 194 NALHVLMSANPLDNGIEPCAFEGVTVFHTRIAEAKLTSVPKGLPPTLLEHLHDYNNKIS 253
Db 133 TMLRNLDSLYNQLHSLGSE--QFRGLR-----KLLSLHURSNLSR 170
QY 254 TVELEDFKRYKELQRLGLGNKKTIDENGSLANIPRVREIHLNENKLNKIPSGL-PELKY 312
Db 171 TIPVRIFQDCRNLELLDLGYNRIRSLARNVFAGMIRLHELHNOFSLKLNALFPRLV 230
QY 313 LQIIFLHNSIARVGVNDPCTVPKMKKSLXSALSIFNNPVKYMWMQPATFCV--LSRM 370
Db 231 LQNLVLOWNKISVIG-----QTMSTWSSSL-ORLDSGNEIEAFS-GPSVFQCVPNLQRL 283
QY 371 SV 372
Db 284 NL 285
  
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Search completed: January 24, 2003, 12:30:51
 Job time : 19 secs

[illegible]

2

[illegible]

QY	6	LLFLIALCSAKPF-----FSPSHIALKNMILKMDTDDDDDDDDDDDDDDDDNSLFPPTREP	61
Db	7	LVSLLALSQALPFEEQGEWFDTLLDGGPFPMANDEASGADTSGVLDPD-----SVTPTYS-	60
QY	62	RSHFPPDLFPMCQGCOCYSRVVHCSDLGLTSVPINIPFDTRMLDLQNNKIKETKENDF	120
Db	61	-----AMCPFGCHURVVQCSDLGLKSVKPEISPDITLLDLQNNDISELRKDDF	110
QY	122	KGTLISGLILNNKKLTKIHKPAFLTTTKLRRLLYLSHNLSEIPLNPKSLAELRIHENK	180
Db	111	KGQLHLYALVLNNKISKIHKAPESLURKLOKLYISKNLHVEIPLNPSLSVLEIHNDR	170
QY	182	VKKIQKDTFKGMNALHVLMSANFLDNNGTEPGAFSGVTVFHRIAEAKLTSVPKGLPPT	240
Db	171	IRKVPKGVFSLRNNNCTEMCGNPLENSGTEPGAFGLKLNLYRISEAKLTGIPKDLPET	230
QY	242	LLELHLDYKNISTVEDEFKRYKELQRLGLGNKIKITDIENGLSIANIPRVREITHLENNKLK	300
Db	231	LNELHLDHNKIQATELDRYSKLYRGLGHHQRIEWIENGSLSLFPTLRHLHDNNKLA	290
QY	302	KTPSGLPKELYLIQIIFLHNSIARVGVNDPCPTVPKMKKLSYSAISLNFNNPKYVWEMOPA	360
Db	291	RYVSPGLDKLIQVYVYLSHNNITKVGVDNFCPMGFGVKRAYNGYKISLNFNNPKYVWEMOPA	350

Db 291 RVPGLPDLKLLQVVYLHSNNITKVGVNDFCPMGFGVKRAYNGIS

F;210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

F:317-369/domain: proceoglycan carboxyl-terminal homology <PC>
F:42,48/Binding site: dermatan sulfate (Ser) (covalent) #status experimental
F:181,199/Binding site: dermatan sulfate (Ser) (covalent) #status predicted
F:271,312/Binding site: carbohydtrate (Asn) (covalent) #status predicted

Query Match 48.6%; Score 969; DB 2; Length 357;
Best Local Similarity 50.0%; Pred. No. 8.9e-59;
Matches 187; Conservative 65; Mismatches 98; Indels

QY	64
Db	46

```

5 VLLLFLALCSAKPFPSPHIALKNMMLKMDTDDDDDDDDDEDSNLSFPTREPRSH
   : : | : | | | | : : : | | : | : | : | : | : | : | : | : | : | : |
6 LFWLLLPVCLATRRFHQK---GLDFDMEIEGSAD-----MAPTDPPVIS

```

Qy 65 FPFDFPWCFFGQCYSRVVHCSDGLTSPVTNIPFTRMLDLQNKKI KEIKENDFKGL 124
- :||| ||| :||| ||| ||| :||| :||| ||| ||| |||
db 47 GRG---PVCPRGCCHLRVVQCSDGLGERVPKDLPDPTLLDLQNKKITEIKEGDFKNL 102

Qy	125	TSLYGLILNNKLTIKIHPKAFLTTKKLRRLYLSHNQLSEIPNLPSKLAEIRIHENKVKK	184
	:	: : :	:
Db	103	KNLHALIIVNKKISKISPAFAFAPKLKRLRYLSKNLKPENPKSLQEIARAHENEWSK	162
	:	: : :	:

Qy 185 IQKDTFGMNAHLVLEMSANPLDNCIEGAFEGV-TVFHRTAEAKLTSVPKGLPPTLL 243

Db 163 LRKAVFNGINOVIVIEIGTNPDKSSGTENGAFQGMKRISYIRADTNITSPKGLPPSLT 222

QY 244 EUHLDYKNISTVELEDFKRYKELQRLGLGNKITDIENGLANIPRVREIHLNKK 303

QY 304 PSLPELXYLQIIIFLHSNSTARVGVNDFCPTVPKMKSLYSAISLIFNNPVKYWEQPATF 363

Qy 364 RCVLSRMSVOLGNF 377
||: | :||:|:

RESULT 6

NB0028
 decorin precursor - human
 N;Alternate names: cartilage proteoglycan protein II; DS-PG II; PG40 core protein; pr
 C;Species: Homo sapiens (man)
 C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #Text_change 21-Jan-2000
 C;Accession: A45016; A45015; A26476; S05640
 R;Vetter, U.; Vogel, W.; Just, W.; Young, M.F.; Fisher, L.W.
 Genomics 15, 161-166, 1993
 A;Title: Human decorin gene: intron-exon junctions and chromosomal localization.
 A;Reference number: A45016; MUID:93162643; PMID:8432527
 A;Accession: A45016

A;Residues: 1-359 <VET>
A;Cross-references: GB:L01125; GB:L01126; GB:L01127; GB:L01128; GB:L01129; GB:L01130;

R; Danielson, K.G.; Fazio, A.; Cohen, I.; Cannizzaro, L.A.; Eichstetter, I.; Iozzo, R. Genomics 15, 146-160, 1993

A;111111: The human decollin gene. INLION EXON ORGANIZATION, DISCOVERY OF TWO ALTERNATIVE
A;Reference number: A45015; MUID:93162642; PMID:8432526
A;Accession: A45015

A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 28-70 <DA2>
A;Cross-references: CH.M00262

A;Note: sequence extracted from NCBI backbone (NCBIP:125013)
A;Accession: B45015

A;Molecule type: DNA
A;Residues: 296-359 <DAN>

R;Krusius, T.; Ruoslahti, E.
Proc. Natl. Acad. Sci. U.S.A. 83, 7683-7687, 1986

A; Reference number: A26476; MUID:87017013; PMID:3484330

A:Accession: A26476
 A:Molecule type: mRNA
 A:Residues: 1-359 <KRU>
 A:Cross-references: GB:M4219; NID:g181169; PIDN:AAB00774.1; PID:g181170
 R:Noughley, P.J.; White, R.J.
 Biochem. J. 262, 823-827, 1989
 A:Title: Dermatan sulphate proteoglycans of human articular cartilage. The properties of
 A:Reference number: S05639; MUID:90073579; PMID:2590169
 A:Accession: S05640
 A:Molecule type: protein
 A:Residues: 31-33, 'X', 35-50 <R0U>
 C:Comment: This protein binds type I collagen.
 C:Genetics:
 A:Gene: GDB:DCN
 A:Cross-references: GDB:119839; OMIM:125255
 A:Map position: 12q21.3-12q23
 A:Introns: 71/1; 108/3; 180/1; 218/1; 249/2; 295/3
 A>Note: The first two introns occur before the initiator codon
 C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat
 C:Keywords: chondroitin sulfate proteoglycan; collagen binding; dermatan sulfate; dupli
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:17-30/Domain: propeptide #status predicted <PRO>
 F:31-359/Product: decorin #status predicted <MP>
 F:48-72/Domain: proteoglycan amino-terminal homology <PAH>
 F:82-105/Domain: leucine-rich alpha-2-glycoprotein repeat
 F:106-125/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:130-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:151-174/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:175-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F:201-221/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F:222-245/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 F:246-269/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
 F:270-293/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
 F:293-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
 F:308-359/Domain: proteoglycan carboxyl-terminal homology <PRC>
 F:34/Binding site: dermatan sulfate (Ser) (covalent) #status experimental
 F:189,325/Binding site: dermatan sulfate (Ser) (covalent) #status predicted
 F:211,262,303/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 48.48; Score 963.5; DB 1; Length 359;
 Best Local Similarity 50.48; Pred. No. 2.1e-58;
 Matches 191; Conservative 65; Mismatches 100; Indels 23; Gaps 4;
 QY 1 MKEYVLLFLALCS-AKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDDDDDNSLFPTR 59
 DB 1 MKATIIILLLAQVSWAGPF---QQQGLDFDFMLEDEASGIGVEVDDRD----- 45
 QY 60 EPRSHFFPDLFPMCPFCQCYSRVVHSGSDGLGTSVPTNIPFDTRMLDLQNNKIKEIKEN 119
 DB 46 -----FFPSLGPVCPFCQCQLRVVQCSGLGLDKVPKDPDPTLLDLQNNKIKEIKDG 99
 QY 120 DFKGLTSYGLILNNKLTIKHPKAFLLTKLRRLYLHSHNLSLPIPLNPKSLAEIRHE 179
 DB 100 DFKNLKLNHALILVNNKISKVSGAFTPLVKLERLYLSKNOLKELPERKMPKTQLRAHE 159
 QY 160 NKVKIKQDKTFKGMNALHVLMSANPLDNNNGIEPGAFGV-TVPHIRIATAKLTSPVKGL 238
 DB 160 NEITKVRKVTENGLNOMIVIELGTNPLKSSGIEGAFQGMKKLYIRIADTNITSIQGL 219
 QY 239 PPTLELHLNDYKISTVELEDFKRYKELQRLGLGNKKITDIENSGLANIPRVRIHLNEN 298
 DB 220 PPSUTELHLDGNKSRVDAASLKGNNLAKLGLSFNSISAVDNGSLANTPHLRHLHDNN 279
 QY 299 KLKKTIPSPKELKYLIQIFLHNSNIVGVNDFCPTVPKMKSLYSATLSFNNPVKWEK 358
 DB 280 KLTRVPGGLAEHKYIQVYLLHNNISVVGSDFCPPGHNTKKASYSGVLSFNSNPVQWEI 339
 QY 359 QPATFRCVLSRMSVOLGNF 377
 DB 340 QPSTFRCVVRSALQNGY 358

RESULT 7

S06280
 decorin precursor - bovine
 N:Alternate names: dermatan sulfate proteoglycan II; proteoglycan core protein II
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Aug-1999
 C:Accession: S06280; B31430; A26545; A20935
 R:Day, A.A.; McQuillan, C.I.; Termino, J.D.; Young, M.R.
 Biochem. J. 248, 801-805, 1987
 A:Title: Molecular cloning and sequence analysis of the cDNA for small proteoglycan I
 A:Reference number: S06280; MUID:88133946; PMID:3435485
 A:Accession: S06280
 A:Molecule type: mRNA
 A:Residues: 1-360 <DNA>
 A:Cross-references: EMBL:Y00712; NID:9618; PIDN:CAA68702.1; PID:g619
 R:Choi, H.U.; Johnson, T.L.; Pal, S.; Tang, L.H.; Rosenberg, L.; Neame, P.J.
 J. Biol. Chem. 264, 2876-2884, 1989
 A:Title: Characterization of the dermatan sulfate proteoglycans, DS-PGI and DS-PGII,
 A:Reference number: A31430; MUID:89123388; PMID:2914936
 A:Accession: B31430
 A:Molecule type: protein
 A:Residues: 31-33, 'X', 35-54 <CHO>
 A:Experimental source: cartilage; fetal skin
 R:Coster, L.; Rosenberg, L.C.; van der Rest, M.; Poole, A.R.
 J. Biol. Chem. 262, 3809-3812, 1987
 A:Title: The dermatan sulfate proteoglycans of bovine sclera and their relationship t
 A:Reference number: A26545; MUID:87137687; PMID:3818667
 A:Accession: A26545
 A:Molecule type: protein
 A:Residues: 31-50 <COS>
 A:Experimental source: sclera
 R:Pearson, C.H.; Winterbottom, N.; Fackre, D.S.; Scott, P.G.; Carpenter, M.R.
 J. Biol. Chem. 258, 15101-15104, 1983
 A:Reference number: A20935; MUID:84087911; PMID:6654908
 A:Accession: A20935
 A:Molecule type: proLein
 A:Residues: 31-54 <PEA>
 A:Experimental source: skin
 R:Chopra, R.K.; Pearson, C.H.; Pringle, G.A.; Fackre, D.S.; Scott, P.G.
 Biochem. J. 232, 277-279, 1985
 A:Title: Dermatan sulphate is located on serine-4 of bovine skin proteodermatan sulph
 nces around glycosylation sites in different proteoglycans.
 A:Reference number: A44700; MUID:86103195; PMID:3936484
 A:Contents: annotation; glycosylation
 C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglyc
 C:Keywords: chondroitin sulfate proteoglycan; collagen binding; dermatan sulfate; ext
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:31-360/Product: decorin #status predicted <PRO>
 F:49-73/Domain: proteoglycan amino-terminal homology <PAH>
 F:83-106/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:107-130/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:131-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F:176-199/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F:202-222/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 F:223-246/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
 F:247-270/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
 F:271-293/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
 F:294-308/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
 F:309-360/Domain: proteoglycan carboxyl-terminal homology <PCB>
 F:34/Binding site: dermatan sulfate (Ser) (covalent) #status experimental
 F:190,326/Binding site: dermatan sulfate (Ser) (covalent) #status predicted
 F:212,263,304/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 47.3%; Score 943; DB 2; Length 360;

Best Local Similarity 49.1%; Pred. No. 5.3e-57;

Matches 186; Conservative 69; Mismatches 102; Indels 22; Gaps 5;

QY 1 MKEYVLLFLALCS-AKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDDDNSLFPTR 59
 DB 1 MKATIIILLLAQVSWAGPF---QQQGLDFDFMLEDEASGIGVEHFEVPEI 48

QY 60 EPRSHFFPDLFPMCPFCQCYSRVVHCSDGLGTSVPTNIPFDTMRMLDQNNKIKEIKEN 119
 Db 49 EP-----MGVPCPRCCHLRVQCSDGLGTSVPTNIPFDTMRMLDQNNKIKEIKOG 100
 QY 120 DFKGLTSLYGLLNNKTKTHPKAFLLTKRLRLYLSSHNLSEIPLNPKSLAEIRIHE 179
 Db 101 DFKNLKNUHTLILNNKISKISPGAFAPLVKRLERLYLSKNQKELPEKMKPTLOELRVHE 160
 QY 180 NKVKIKQDTEFGMNAHVLSEANPLDNGIEGAFEGV-TVFHRIAEAKLTSVPKGL 238
 Db 161 NEITKVRKSVENGLNQMLVVELGTNPLKSSGIENGAFQGMKLSYIRIADNTNITIPQGL 220
 QY 239 PPTLLEHLDYNKISTVELEDFKRYKELORLGLGNKNTDIENGSLANIPRVREIHLNEN 298
 Db 221 PPSLTELHLDGKNTKVDAAISLKLNNLAKLGLSFNSAVDNGSLANTPHLRELHLNEN 280
 QY 299 KLKKTIPSGLPKLYLOIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSIFNPNPKYWEW 358
 Db 281 KLAKVPGVADHKYIQVYVYLNHNNTSAGNSDFCPGTYNTKASYSVGLSFNSPVOYWEI 340
 QY 359 QPATRCVLSRMSVOLGNF 377
 Db 341 QPSTFCVYVRAAOLGNV 359
 RESULT 8
 147020
 decorin - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 20-Aug-1999
 C:Accession: I47020
 R:Zhan, Q.; Burrows, R.; Cintron, C.
 Invest. Ophthalmol. Vis. Sci. 36, 206-215, 1995
 A:Title: Cloning and in situ hybridization of rabbit decorin in corneal tissues.
 A:Reference number: I47020; MUID:95122319; PMID:7822148
 A:Accession: I47020
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-360 <ZNA>
 A:Cross-references: GB:S76584; MID:g913374; PIDN:AAAB33083.1; PID:g913375
 C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology: proteoglycan
 F:49-73/Domain: proteoglycan amino-terminal homology <PAH>
 F:83-106/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:107-130/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:131-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F:176-199/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F:202-223/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 F:223-246/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
 F:247-270/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
 F:271-293/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
 F:294-308/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
 F:309-360/Domain: proteoglycan carboxyl-terminal homology <PCH>
 Query Match 47.2%; Score 941; DB 2; Length 360;
 Best Local Similarity 49.6%; Pred. No. 7.3e-57;
 Matches 188; Conservative 67; Mismatches 102; Indels 22; Gaps 5;
 QY 1 MKEYVLLFLALCS-AKFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDSLFPTR 59
 Db 1 MTATLILLALLAQVSNAGFF---QQRGLDFMED-EASGIGDERAPEPLDLM----- 50
 QY 60 EPRSHFFPDLFPMCPFCQCYSRVVHCSDGLGTSVPTNIPFDTMRMLDQNNKIKEIKEN 119
 Db 51 -----LGPVCPFCCHLRVQCSDGLGTSVPTNIPFDTMRMLDQNNKIKEIKOG 100
 QY 120 DFKGLTSLYGLLNNKTKTHPKAFLLTKRLRLYLSSHNLSEIPLNPKSLAEIRIHE 179
 Db 101 DFKNLKNUHTLILNNKISKISPGAFAPLVKRLERLYLSKNHKLPEKMKPSLQELRAHE 160
 QY 180 NKVKIKQDTEFGMNAHVLSEANPLDNGIEGAFEGV-TVFHRIAEAKLTSVPKGL 238
 Db 161 NEITKVRKSVENGLNQMLVVELGTNPLKSSGIENGAFQGMKLSYIRIADNTNITIPQGL 220

QY 239 PPTLLEHLDYNKISTVELEDFKRYKELORLGLGNKNTDIENGSLANIPRVREIHLNEN 298
 Db 221 PPSLTELHLDGKNTKIDASSLSKLNNLAKLGLSFNSAVDNGSLANAPHLRELHLNEN 280
 QY 299 KLKKTIPSGLPKLYLOIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSIFNPNPKYWEW 358
 Db 281 KLIRVPGGADHKYIQVYVYLNHNNTSVGANDFCPPGYNTKASYSVGLSFNSPVOYWEI 340
 QY 359 QPATRCVLSRMSVOLGNF 377
 Db 341 QPSTFCVYVRAIOLGNV 359
 RESULT 9
 A55454
 decorin precursor - mouse
 N:Alternate names: proteoglycan II
 C:Species: Mus musculus (house mouse)
 C:Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 20-Aug-1999
 C:Accession: A55454; S20812
 R:Scholzen, T.; Solursh, M.; Suzuki, S.; Reiter, R.; Morgan, J.L.; Buchberg, A.M.; S1
 J. Biol. Chem. 269, 28270-28281, 1994
 A:Title: The murine decorin. Complete cDNA cloning, genomic organization, chromosomal
 A:Reference number: A55454; MUID:95050610; PMID:7961765
 A:Accession: A55454
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-354 <SCH>
 A:Cross-references: GB:X53929; MID:g53668; PIDN:CAA37876.1; PID:g53669
 R:Naitoh, Y.; Suzuki, S.
 submitted to the EMBL Data Library, July 1990
 A:Description: Nucleotide sequences of cDNAs encoding mouse PGI and PGII.
 A:Reference number: S20811
 A:Accession: S20812
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-354 <NAI>
 A:Cross-references: EMBL:X53929; MID:g53668; PIDN:CAA37876.1; PID:g53669
 C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology: proteoglyc
 C:Keywords: collagen binding; extracellular matrix; glycoprotein
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:17-30/Domain: propeptide #status predicted <PRO>
 F:43-67/Domain: proteoglycan amino-terminal homology <PAH>
 F:77-100/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:125-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F:170-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F:196-216/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 F:217-240/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
 F:241-264/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
 F:265-287/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
 F:288-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical
 F:303-354/Domain: proteoglycan carboxyl-terminal homology <PCH>
 Query Match 45.6%; Score 907.5; DB 2; Length 354;
 Best Local Similarity 52.0%; Pred. No. 1.4e-54;
 Matches 170; Conservative 65; Mismatches 87; Indels 5; Gaps 2;
 QY 56 FPTREPSHFPPFD---LFPMPGFCQCYSRVVHCSDGLGTSVPTNIPFDTMRMLDQNN 111
 Db 27 FMLEDASGIIPDPNPNPLSMCPYRCQCHLRVQCSDGLGTSVPTNIPFDTMRMLDQNN 86
 QY 112 KTEIKENDFKGLTSLYGLLNNKTKTHPKAFLLTKRLRLYLSSHNLSEIPLNPKS 171
 Db 87 KITEIKEGAFKNLKDLHTLLVNNKISKISPEAFKPLVKRLERLYLSKNQKELPEKMPRT 146
 QY 172 LAELRHENKVKIKQDTEFGMNAHVLSEANPLDNGIEGAFEGV-TVFHRIAEAK 230
 Db 147 LOELRHENHETIKRSDFNGLNVLVIELGPNKNSGIENGAFQGLKSLYSIRISDTN 206
 QY 231 LTSVPKGLPPTLLEHLDYNKISTVELEDFKRYKELORLGLGNKNTDIENGSLANIPRV 290

[illegible][illegible]

C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 24-Sep-1999
 C:Accession: A46743; A35379
 R:Funderburgh, J.L.; Funderburgh, M.L.; Brown, S.J.; Vergnes, J.P.; Hassell, J.R.; Mann, J. Biol. Chem. 268, 11874-11880, 1993
 A:Title: Sequence and structural implications of a bovine corneal keratan sulfate proteoglycan
 A:Reference number: A46743; MUID:93280153; PMID:8099356
 A:Accession: A46743
 A:Molecule type: mRNA
 A:Residues: 1-342 <FUN>
 A:Cross-references: GB:L11063; NID:g163266; PIDN:AAA30608.1; PID:g163267
 R:Funderburgh, J.L.; Conrad, G.W.
 J. Biol. Chem. 265, 8297-8303, 1990
 A:Title: Isoforms of corneal keratan sulfate proteoglycan.
 A:Reference number: A35379; MUID:90243714; PMID:2139877
 A:Accession: A35379
 A:Molecule type: protein
 A:Residues: 19-36 <FU2>
 A:Experimental source: cornea
 C:Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology
 C:Keywords: glycoprotein; tandem repeat
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-342/Product: lumican #status predicted <MAT>
 F:92,131,164,256/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.38; Score 384; DB 2; Length 342;
 Best Local Similarity 32.2%; Pred. No. 6.3e-19;
 Matches 101; Conservative 68; Mismatches 123; Indels 22; Gaps 10;

QY 66 PFDFLDF---PWCFFGQCQ---YSRVVHCSDLGLTSVPTNIPFDTMLDLQNNKIKEIKENDFKGLT 118
 DB 29 FFOALYGRSSNCAPECNCPESYAMVCDLKLKSVPM-VPPGIKYLRLNNQIDHDD 87

QY 119 NDFKGLTSLYLILNNKLL--TKIHPKAFUTTKRLRLYLHNSLSTIPLNLPKSLAELR 176
 DB 88 KAFENVTDQLWLDHNLLENSKIKGVFVKLQKLLHINYNNLTESVGLPKSLVDLQ 147

QY 177 IHENKVKIKQDTPKGMNALHVLMSANPLDNGIEPAGFEGV-TVPHIRIAEAKLTSVP 235
 DB 148 LTNNKISKLL--GSFDGLVNLTFIHLQNLKEDAVS-AALKGLKSLLEYLDLSFNQMTKLP 204

QY 236 KGLPTLLELDYKNTSTVELEDFKRYKELQRLGLGNKKITDI-ENGSLANIPRVREIH 294
 DB 205 SGLPVSLLTLYLDNNKISINIDPEFFKRSALQYLRSHNELADSGVPGNSFNVSLLLED 264

QY 295 LENNLKPKIPSGLPPELK--YLQIIFLHNSIARVGVNDPCTVPKMKKSYSAISLFNPP 352
 DB 265 LSYNKLKSIPTVNNENLYLEV-----NELEKFDVKSFCKILGLPLSYSKIKHLRLDGNH 319

QY 353 VKYVEMQAPATRCV 366
 DB 320 ITQTSLLPDMYECL 333

RESULT 13
 S52284
 lumicon, secretory interstitial proteoglycan precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 24-Sep-1999
 C:Accession: S52284
 R:Krull, N.B.
 submitted to the EMBL Data Library, January 1995
 A:Reference number: S52284
 A:Accession: S52284
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-338 <KRU>
 A:Cross-references: EMBL:X84039; NID:g643023; PIDN:CAA58858.1; PID:g643024
 C:Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology

Query Match 19.0%; Score 378; DB 2; Length 338;
 Best Local Similarity 32.2%; Pred. No. 1.6e-18;
 Matches 99; Conservative 67; Mismatches 123; Indels 18; Gaps 9;

QY 69 DLFPMCPFGQCQ---YSRVVHCSDLGLTSVPTNIPFDTMLDLQNNKIKEIKENDFKGLT 125
 DB 32 ELSNCAPECNCPESYAMVCDLKLKSVPM-VPPGIKYLRLNNQIDHIDKAFENV 90

QY 126 SLYGLILNNKLL--TKIHPKAFUTTKRLRLYLHNSLSEIPLNLPKSLAELRIHENKVK 183
 DB 91 DLQWLILDHNLLENSKIKGVFVKLQKLLHINYNNLTESVGLPKSLQDLQLANNKIS 150

QY 184 KICKDTPKGMNALHVLMSANPLDNGIEPAGFEGV-TVPHIRIAEAKLTSVPKGLPPTL 242
 DB 151 KL--GSFDGLVNLTFIHLQNLKEEAVS-ASLKGKLSLEYLDLSFNQMSKLPAGLITSL 207

QY 243 LEHLDYKNTSTVELEDFKRYKELQRLGLGNKKITDI-ENGSLANIPRVREIHLENNKIL 301
 DB 208 LTYLDNNKITNIPDEYFNKRTGLQYLRSHNELADSGVPGNSFNISSELDLDSYNKIL 267

QY 302 KIPSGLPPELK--YLQIIFLHNSIARVGVNDPCTVPKMKKSYSAISLFNPPVKYVEMQ 359
 DB 268 SIPTVNNENLYLEV-----NKLEKFDVKSFCKILGLPLSYSKIKHLRLDGNPLTQSSLP 322

QY 360 PATFRCV 366
 DB 323 PMYECL 329

RESULT 14
 I39068
 proline- arginine-rich end leucine-rich repeat protein PRELP precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 24-Sep-1999
 C:Accession: I39068
 R:Bengtsson, E.; Neame, P.J.; Heinigard, D.; Sommarin, Y.
 J. Biol. Chem. 270, 25639-25644, 1995
 A:Title: The primary structure of a basic leucine-rich repeat protein, PRELP, found i
 A:Reference number: I39068; MUID:96029653; PMID:7592739
 A:Accession: I39068
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-382 <RES>
 A:Cross-references: EMBL:U29089; NID:g886135; PIDN:AAC50230.1; PID:g886136
 C:Genetics:
 A:Gene: GDB:PRELP
 A:Cross-references: GDB:696218
 A:Map position: lq32.1-lq32.1
 C:Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology
 C:Keywords: tandem repeat

Query Match 18.0%; Score 358.5; DB 2; Length 382;
 Best Local Similarity 30.7%; Pred. No. 4e-17;
 Matches 90; Conservative 55; Mismatches 133; Indels 15; Gaps 7;

QY 47 DDDDENSLFTPREPSHFFPDLFPMCPFGQCQ---YSRVVHCSDLGLTSVPTNIPFDT 103
 DB 50 DEPAETDLPPLPPG---PPSIFFDCPRECYCPDPFSAIYCDNRNLKVPV-IPPRI 104

QY 104 RMLDLQNNKIKEIKENDFKGLTSLYLILNNKILKIHKAPLFTTKLRLRLYLSHNSLSE 163
 DB 105 HYLYLQNNFITELPVESEFONATGLRWLNLDNNRIRKIDQVLEKLPGLVFLYMEKNQLEE 164

QY 164 IPLNLPKSLAELRIHENKVKIKQDTPKGMNALHVLMSANPLDNGIEPAGFEGV-TVF 222
 DB 165 VPSALPRLNLEQLRSLNSHISIPPGVFSKLENLLLDLQHLRLSDGVFKPDPPTFHGLKNLM 224

QY 223 HIRIAEAKLTSVPKGLPPTLLEHLHDYKNTSTVELEDFKRYKELQRLGLGNKKITDI-IE 280
 DB 225 QLNLAHNLIRKMPRVPTAIHQYLDLSNKIETIPNGYKSPFNLAFLRLNLYNKILDRGLP 284

QY 281 NGSLANIPRVREIHLENNKILKIPSGLPPELKYLQIIFLHNSIARVGVNDPFCP 333
 DB 285 KNSF-NISNLLVLHLHSHNRISVPAINNRLHL---YLNNSNIEKINQTCPCP 333

QY 223 -----HTR---IAEAK----- 230
 Db 209 TLRHSHNYCDCHLAWLSDWLRQRTTIGQFTLCMAPVHLRGFSVADVQRKEYVCYCPGPHS 268
 QY 231 -----LTSVPKGLPPTLLEHLHDYNNKISTVELEDFK 261
 Db 269 EAPACNANSLSPACSCSNIVDCRGKGLUFEIPANLPEGIVEIRLEQNSIKSPAGAFI 328
 QY 262 RYKELQRLGLGNKKTIDTENGSLANIPRVREIHLNENKAKIPSGLPE-LKYIQIIFLHS 320
 Db 329 QYKCLKRIDISKNQISDIADPAFOGLKSLTSLVLYGNKITEIPKGLFDGLVSLQLLLLNA 388
 QY 321 NSIARVGVNDPCVPVKMKKSLYSALSIFNNPVK 354
 Db 389 NKINCLRWNTF-----QDLQNLNLLSLYDNKIQ 416
 RESULT 18
 T42218
 slit-1 protein homolog - rat
 N:Alternate names: MEGF4 protein
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2002
 C:Accession: T42218
 R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
 Genomics 51, 27-34, 1998
 A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
 A:Reference number: 214126; MUID:98360089; PMID:9693030
 A:Accession: T42218
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1531 <NAK>
 A:Cross-references: EMBL:AB011530; NID:g3449289; PIDN:BAA32460.1; PID:g3449290
 A:Experimental source: strain Sprague-Dawley; brain
 C:Genetics:
 A:Gene: MEGF4
 C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein

Query Match 16.2%; Score 323; DB 2; Length 1531;
 Best Local Similarity 25.0%; Pred. No. 6.4e-14;
 Matches 98; Conservative 64; Mismatches 116; Indels 114; Gaps 10;

QY 74 CPFGCQSVRVVHCSDLGTSVTPNIPEDT-----RMDL 108
 Db 282 CPAMCSCSNGIVDCRGKGLTAIPANLP-ETMTEIRLELNGIKSTPPGAFSPYKLRRLD 340
 QY 109 QNNKIKEIKENDFKGLTSLYGLIINNKKLTKIHPKAFITTKLRRLYLSHNSLSEI---P 165
 Db 341 SNNQIAELAPDAFOGLRSLNSLVLYGNKTTDLPRGVFGLYTLQLLLNANKINCIRPDA 400
 QY 166 LNLPKSLAELRIHENKVKYKIQDFTKGMNALHVLMSANP-----LDNNGIE 212
 Db 401 FQDLQNLNLLSLYDNKIQSLAKGFTSLRAITQLHLAQNPFICDNLKWLADFLRTNP 460
 QY 213 -PGA-----FEGVTVEH----- 223
 Db 461 TTGARCASPRLANRIGQIKSKFRCSAKEQYFIPGTEYHLNSETSDVACPHKCRCE 520
 QY 224 ---TRIAEAKLTSVPKGLPPTLLEHLHDYNNKISTVELED-FKRYKELQRLGLGNKKTIDI 279
 Db 521 ASVVECSGLKLSKIPERIPQSTTELRLNNNEISILEATGLFKLHLKLNLSNNKVS 580
 QY 280 ENGLSNIAPRVREIHLNENKLLKIPSGL-PELKYIQIIFLHSNIARVGVNDPCVPVKM 338
 Db 581 EDGTFEGATSVSELHLTANQLSVRSQMFRLGLDGLRTIMLRNNRISCIHNDSETGLRNV 640
 QY 339 KKSLY-----SAISIFNNP 352
 Db 641 LLSLYDNHITTSFGAFDTLQALSTLNLNLP 672

RESULT 19
 S55275

fibromodulin precursor - human
 N:Alternate names: 59K collagen-binding matrix protein
 C:Species: Homo sapiens (man)
 C:Date: 23-Aug-1995 #sequence_revision 03-Oct-1995 #text_change 24-Sep-1999
 C:Accession: S55275; S35710; S32752; S41925
 R:Hildebrand, A.; Romaris, M.; Rasmussen, L.M.; Heinegard, D.; Twardzik, D.R.
 Biochem. J. 302, 527-534, 1994
 A:Title: Interaction of the small interstitial proteoglycans biglycan, decorin and fi
 A:Reference number: S55275; MUID:94379985; PMID:8093006
 A:Accession: S55275
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-376 <HI2>
 A:Cross-references: EMBL:X75546; NID:g453156; PIDN:CAA53233.1; PID:g453157
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
 R:Antonsson, P.; Heinegard, D.; Oldberg, A.
 Biochim. Biophys. Acta 1174, 204-206, 1993
 A:Title: Structure and deduced amino acid sequence of the human fibromodulin gene.
 A:Reference number: S35710; MUID:93363641; PMID:8357838
 A:Accession: S35710
 A:Molecule type: DNA
 A:Residues: 1-3, 'T', 5-86, 'P', 88-209, 'N', 211-225, 'Y', 227-343, 'Q', 345-354, 'M', 356-362, '
 A:Cross-references: EMBL:X72513; NID:g297090; PIDN:CAA51418.1; PID:g297091
 C:Comment: Keratan sulfate can be covalently attached to N-acetylglucosamine at the a
 C:Genetics:
 A:Gene: GDB:FMOD
 A:Cross-references: GDB:228979; OMIM:600245
 A:Map position: 1q32.1-1q32.1
 A:Introns: 326/2
 C:Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology
 C:Keywords: cartilage; chondroitin sulfate proteoglycan; collagen binding; connective
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-376/Product: fibromodulin #status predicted <MAT>
 F:38,39,42,45,47,50,53,55,63,65/Binding site: sulfate (Tyr) (covalent) #status predic
 F:127,166,201,291/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.0%; Score 318; DB 2; Length 376;
 Best Local Similarity 26.1%; Pred. No. 2.2e-14;
 Matches 86; Conservative 65; Mismatches 131; Indels 48; Gaps 9;

QY 63 SHFFPFDLPF-----CPFGCQ-----YSRVHWCSDLG 91
 Db 37 TYDYPDYPYETPEYPPYGVDEGPAYTVGSPDPDPDCECCDPNFLTAMVCDNRN 96
 QY 92 LTSVTPNIPDTRMLDQNNKIKEIKENDFKGLTSLYGLIINNKKLT--KIHPKAFITTK 149
 Db 97 LKYLPP-VPSPKMYVFNQNTISOEGVFDNATGLLWIALHGNQITSDKVGKVFESKLR 155
 QY 150 KLRRLYLSHNSLSEIPLNLPKSLAELRIHENKVKIKQDFTKGMNALHVLMSANPLDNN 209
 Db 156 HLERYLDHNLTTRMPGLPRLSLRELHLHDHNSIRVNNALLEGLENLTALYLQHDIEQEV 215
 QY 210 GTEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTLLEHLHDYNNKISTVELED-FKRYKELQR 268
 Db 216 G---SSMRGLRSLIILLDSYNHLRKVPDGLPSALEQLYMEHNNVYTPDSYFPGAPKLLY 272
 QY 269 LGGNKKITDIENGSLA-----NIPRVREIHLNENKLLKIPSGLPELKYIQIIFLHSNSTA 324
 Db 273 VRLSHNSLT---NGLASNTFSSSLLLELDLSYNQLOKIP---PVNTLNENLYLQGNRIN 326
 QY 325 RGVGVNDPCFTVPKMKKSLYSALSIFNNPVK 354
 Db 327 EFSISFCTVVDVNVNFSKLQVVRDLGNEIK 356

RESULT 20
 B36665
 slit protein 2 precursor - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
 C:Accession: B36665
 R:Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
 Genes Dev. 4, 2169-2187, 1990

QY 207 -----DNNIGBGA-----FEQVTFHRI 226
 Db 253 PYTCQSPSQLKGNVADLHQEFKCSGLTEHAPMECGAENSCPHPCRCADGI-----VDC 308
 QY 227 AEAKLTSPKGLPTLLEHLDYKNTSTVELEDFKRYKELQRLGLGNKTKITDIENGLAN 286
 Db 309 REKSLTSVPVTLPTDITDVRLEQNFITELPPKSFSSFRRLRDLNNNISRTAHDAISG 368
 QY 287 IPRVREIHLNENKUKK1PSGL-PELKYLIQIIFLHNSIARVGVNDCEPTVPKMKKSLY-- 343
 Db 369 LKQTLTIVLYCNKIKDLPVGFGLSGRLRLLLNANEISCIKRDAP-----RDHLSL 420
 QY 344 SAISLPNNPVKYWMQPAFTFCVLSRMSVOL 374
 Db 421 SLLSLYDNNIQ--SIANGTFDAMKSMKTVHL 449

RESULT 22
 A58532
 C:Species: Mus musculus (house mouse)
 C:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 05-Nov-1999
 C:Accession: A58532
 J. Suzuki, Y.; Sato, N.; Tohyama, M.; Wanaka, A.; Takagi, T.
 A:Title: CDNA cloning of a novel membrane glycoprotein that is expressed specifically in
 A:Reference number: A58532; MUID:96394313; PMID:8798419
 A:Accession: A58532
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1091 <SUZ>
 A:Cross-references: GB:D8752; NID:g1545806; PIDN:BAAL1416.1; PID:g1545807
 C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan amino-ter
 F:36-61/Domain: proteoglycan amino-terminal homology <PA>
 F:71-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:95-117/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:118-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:142-165/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F:166-189/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F:191-213/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 F:214-237/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
 F:238-261/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
 F:262-285/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
 F:286-309/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
 F:310-333/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
 F:334-357/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
 F:358-381/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
 F:385-408/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
 F:409-432/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
 F:440-485/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match 14.9%; Score 296; DB 2; Length 1091;
 Best Local Similarity 30.1%; Pred. No. 2.8e-12;
 Matches 94; Conservative 64; Mismatches 124; Indels 30; Gaps 12;

QY 74 CPFGCCYRVVHSGDGLSVPTNIPFDTMIDLQNNKTEKENDFKGLTSLYGLIN 133
 Db 43 CAAACTCAGNSLDCSGRLATLPDLPSWTRSLNLSYNRLSEIDSAFEDLTNLQEVYL 102
 QY 134 NKLTKTHPKAFLTKRLRLYLHNSNLSI--PMLPKSLAEFLRHENKVKIKQKDF 190
 Db 103 SNEUTAI-PSLGTASIGVSLFLOHNNKILSDGQSUKSYSLVDLSSNNITEIRSSCF 161
 QY 191 KGMNALHVLMSANPLDNNGI--EPGAFEGV--TVPHIRIAEAKLTSPV-KGLP-PTLL 243
 Db 162 P--NGLRIRELN--LASNRITLESAGFDGLSRSLTLRLSKNRITQLPVKAFKPLRT 216
 QY 244 ELHLDYKNTSTVELEDFKRYKELQRLGLGNKTKITDIENGLANIPRVREIHLNENKUKK 303
 Db 217 QLDLNRNRIRLIEGLTFQGLSDSLVLRQNRNITSLRTDGAFWGLSKMHVHLHLEVNSIVE 276
 QY 304 PSG-LPELKYLIQIIFLHNSIARVGVN--DFCPTVPKMKKSLYSALSIFLNNPVKYWMQ 360

Db 277 NSGSLYGLTALHQLHLSNNSISRIQDQWSEFC-----QKLHELLISFNLLTRDESL 329
 QY 361 ATRFCVLSRMSV 372
 Db 330 AE----LSSLSI 337

RESULT 23
 A53860
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Nov-1999
 C:Accession: A53860
 R. Neame, P.J.; Sommer, Y.; Boynton, R.E.; Heinemann, D.
 J. Biol. Chem. 269, 21547-21554, 1994
 A:Title: The structure of a 38-kDa leucine-rich protein (chondroadherin) isolated fro
 A:Reference number: A53860; MUID:94342341; PMID:8063792
 A:Accession: A53860
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-361 <NEA>
 A:Cross-references: GB:U08018; NID:g470671; PIDN:AAA21330.1; PID:g470672
 C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan carbox
 C:Keywords: disulfide bond
 F:300-346/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match 14.8%; Score 294; DB 2; Length 361;
 Best Local Similarity 27.5%; Pred. No. 9.2e-13;
 Matches 78; Conservative 58; Mismatches 106; Indels 42; Gaps 10;

QY 74 CPFGCCYRVVH--CSDLGLTSPVTNIPFDTMIDLQNN----- 111
 Db 25 CPQNCCHSDLOHVICDKVGLQKIP-KVSEKTKLLNQRNFPVLTATNSFRAMPNLVSLH 83
 QY 112 ----KIKEIKENDFKGLTSLYGLINNNKLTPIHPKAFLTTKRLRYLSHNLQSEIPLN 167
 Db 84 LOHCITREVAAGAFGLKQLIYLYLHNDIRVLRAGAFDDLTLYLYLHDKVTELPGR 143
 QY 168 LPSKLAEE--LRHFNKVKIKQKDFKGMNALHVLMSANPLDNNIGPEGAFEGV-TVFH 223
 Db 144 LSLPLNFILOLNNKIRELSGAFQAKDLRWLYLSENSL--SSLOPGALDDVENLAK 201
 QY 224 IRIAEAKLTSPVKGPLPTLL---ELHLDYKNTSTV---ELEDKRYKELQRLGLGNKTKIT 277
 Db 202 FYLDRNLSSYPSAALSRLRVVEELKLSHNPLKSPIDNAFQSGRY--LETLLDNTNLE 259
 QY 278 DIENGLANIPRVREIHLNENKUKKIPSGLPPELKYLIQIIFLHNS 321
 Db 260 KFDGAFGLVTTLRKHVHLNENRHLQPSNFP-FDSLETTLTLTN 302

RESULT 24
 T42626
 C:Species: Mus musculus (house mouse)
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 16-Aug-2002
 C:Accession: T42626
 R. Holmes, G.P.; Neagus, K.; Burrridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.
 Mech. Dev. 79, 57-72, 1998
 A:Title: Distinct but overlapping expression patterns of two vertebrate slit homologs
 A:Reference number: 222177; MUID:99279238; PMID:10349621
 A:Accession: T42626
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1025 <HOL>
 A:Cross-references: EMBL:AF074960; NID:g4151258; PID:g4151259; PIDN:AAD04345.1
 C:Genetics:
 A:Gene: Slit2
 C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein

A;Reference number: JC6128; MUID:96413591; PMID:8816745

A;Accession: JC6128

A;Molecule type: DNA

A;Residues: 1-603 <BOI>

C;Cross-references: GB:U66900; NID:g1621612; PIDN:AAB17270.1; PID:g1621613

C;Comment: This protein is a serum protein and it is of the ternary complex

C;Genetics:

A;Gene: als

A;Map position: 17

Query Match 13.3%; Score 265; DB 2; Length 603;

Best Local Similarity 27.6%; Pred. No. 1.7e-10;

Matches 88; Conservative 64; Mismatches 103; Indels 64; Gaps 12;

QY 102 DTRMLDLNNKIKKIKENDEKFGTSLTSLVGLLNNNKTKIHPKAFLLTKKLRRLYLSHNOL 161

DB 219 ELRELDLSRNALSVKAVNFIHLPRLOKLYLDRLNLTAVAPRAFLGKMKALRWLDLSHNRV 278

QY 162 SEI-----PINL-----PKS-----LAEIRIHENKVKKIKQDTEFGMN 194

DB 279 AGLEEDTFPGLLGLHVLRLAHNAITSLRPRTFKDLHFLLEQLGHNRIRQLGKTEFGLG 338

QY 195 ALHVLMSANPLDNGIEPCAFGVTVFHIRIAEK---LTSPV---KGLPPTLLEHL 247

DB 339 QLEVLTLNDNQI--HEYKVGAFG--LFNVAVMNLSCNCLRSLEPHVFOGL-GRULSHLH 393

QY 248 DYNKISTVELEDFKRYKELQRLGLGNKKTIDENGSLANIPRVRETHLENNKIKTP--- 304

DB 394 EHSCGLGIRLHTTAGLSGLRLFLRDNSTSSIEQSLAGLSLELDELDTANQTLHLPROL 453

QY 305 -SGLPELKYLIQIIFLHNSIARVGVNDPFC-----TVPKMKKSLYSA----- 345

DB 454 FOGLGQLEYL---LLSNQTLMLSEDVLGPLQRAFWLDLSHNRLETPAEGLFSSGLRLRY 510

QY 346 ISLFNNPVKYWEMQATFR 364

DB 511 LNLNRNSLQTFVFPQGLER 529

RESULT 28

TL13174

gp150 protein - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C;Accession: T13174

R;Tian, S.S.; Zinn, K.

J. Biol. Chem. 269, 28478-28486, 1994

A;Title: An adhesion molecule-like protein that interacts with and is a substrate for a

A;Reference number: Z17630; MUID:95050638; PMID:7961789

A;Accession: T13174

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1051 <TIA>

A;Cross-references: EMBL:U15220; NID:g595859; PID:g595860; PIDN:AAA61796.1

A;Experimental source: strain Oregon R

C;Genetics:

A;Cross-references: FlyBase:FBgn0013272

A;Map position: 2

Query Match

Best Local Similarity 13.3%; Score 265; DB 2; Length 1051;

Matches 98; Conservative 51; Mismatches 146; Indels 66; Gaps 12;

QY 35 EDTDDDDDDDDDDDD---DEDNSLFTPREPRSHFFEDLFPMCPFCQCYSR-----VVH 86

DB 203 EGLDDDDDDDDAADDLLTDDDEQVVFSDVP-----CPFCQCARNVNSYLVA 250

QY 87 CS-----DLGTSVPTNIPF-----DTRMLDLQNNKIKIKEN 119

DB 251 CSRLDMGIQKFGSDITDLVTVNVPKYPILMGPNFQNLGKNVASIKTANCTLEYLHAE 310

QY 120 DFKGLTSLYGLIILNNKTKIHPKAFLLTKKLRRLYLSHNOLSEIP-----LNLPKSLAE 175

DB 311 AFHGLNELYAVNLTDVGLAIINPDTFVGNKKRLMLTISGNDLSVMSSIHLLKSSSIEEL 370

QY 176 RIHENKVKKIQKDTFKGMNALHVLMSANPLDNGIEPCAFGVTVF-HIRIAEAKLTSV 234

DB 371 DFSRNNMELNPKAFSHLSNVVYINLQNSLKK--LPEKAFKTYLLEEDLSVNSLTEL 428

QY 235 PKGL--PPTLELHLDYLNKISTVELEDFKRYKELQRLGLGNKKTIDENGSLANIPRVRE 292

DB 429 PRDIFNGTTLTSLHLKYN--TFNGDLHFGTKDLQQLDLSFNSIVQVHHSFMDKMPGLTN 485

QY 293 IHLNNKIKKI-PSGLPELKYLIQIIFLHNSIARVGVNDPFCPTVPKMKKSLYSAISLFINN 351

DB 486 LNLKNGIKKIQDPSFUTLKLNRHIDLSINDLDQISGMJF-----FKNSELDVIRLNDN 539

QY 352 P 352

DB 540 P 540

RESULT 29

JG0193

G protein-coupled receptor FEX - mouse

C;Species: Mus musculus (house mouse)

C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000

C;Accession: JG0193

R;Hermey, G.; Methner, A.; Schaller, H.C.; Hermans-Borgmeyer, I.

Biochem. Biophys. Res. Commun. 254, 273-279, 1999

A;Title: Identification of a novel seven-transmembrane receptor with homology to glyc

A;Reference number: JG0193; MUID:99121227; PMID:9920770

A;Accession: JG0193

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-907 <HER>

Query Match 13.1%; Score 261.5; DB 2; Length 907;

Best Local Similarity 21.8%; Pred. No. 5e-10;

Matches 99; Conservative 68; Mismatches 127; Indels 161; Gaps 14;

QY 69 DLFPN-CPFGQCQY--SRV---VHCSDGLTSTVPTNIPDTRMLD----- 107

DB 28 DAIPRGCFSHCHCELDGRMLLRVDCSDGLSELPSNLSVFTSYLDLSMNNISQLPASLH 87

QY 108 -----LONNKIKEIKENDPKGLTSLYGLILNN 134

DB 88 RLCCFLEELRLAGNALTHIPKGAFTGLHSLKVLMLQNNQLRKVPBEALQNLRSLSQLRLDA 147

QY 135 NKLTKIHPKAFLLTKKLRRLYLHSHNQLSEIPLNLPKSLAELR----- 176

DB 148 NHISYVPPSCFSGHSLRHLWLDNALDVPVQAFRSLSALQAMTLALNKIHHIADYAFG 207

QY 177 -----IHENKVKKTQKDTFKGMNALHVLMSANPLD-----NN 209

DB 208 NLSSLVVHLHNNRIHSLGKKCFDGLHSLFTLDLNNYNNLDEFPTAIKTLNKLKELGFHSN 267

QY 210 GT-----EPGAFGVTVFVH----- 223

DB 268 NIRSIPERAFVGNPSLITHEFDNPIQFVGVSFAFOHLPRLTLTLNGASHITEFPHTGT 327

QY 224 -----IRIAEAKLTSVPKGL---PPTLLELHLDYLNKISTVELEDFKRYKELQRLGLGNKK 275

DB 328 ATLESLTGTGAKISSLPQAVCDQLPNQVLDLSYNLLE--DLPSLSGCQKLOKIDLRHNE 385

QY 276 ITDIENGSLANIPRVRETHLENNKIKKI-PSGLPELKYLIQIIFLHNS---SIARVGVND 331

DB 386 IYEIKGSTFQQLFNRLSNLANLAWNKIATHPNAFTSLPSLKLKLDLSNLLSFPVTLGLHL 445

QY 332 CPTVPKMKKSLYSAISLFINN-PKYEMQATFR 365

DB 446 THLKLTGNRALQSLPSANFPPELKIEM-PSAYQC 479

RESULT 30

TI9939

[illegible]

RESULT 33

S72271
 proteoglycan Lb precursor - mouse
 N:Alternate names: chondroitin/dermatan sulfate proteoglycan
 C:Species: Mus musculus (house mouse)
 C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 20-Jun-2000
 C:Accession: S72271
 R:Kurita, K.; Shinomura, T.; Ujita, M.; Zako, M.; Iwata, H.; Kimata, K.
 Biochem. J. 318, 909-914, 1996
 A:Title: Occurrence of PG-Ib, a leucine-rich small chondroitin/dermatan sulphate proteoglycan in the skin of the mouse.
 A:Reference number: S72271; MUID:96433109; PMID:8836137
 A:Accession: S72271
 A:Molecule type: mRNA
 A:Residues: 1-322 <CUR>
 A:Cross-references: EMBL:D78274; NID:g1620004; PIDN:BAAL1337.1; PID:g1620005
 A:Experimental source: strain BALB/c; newborn; epiphyseal cartilage
 C:Function:
 C:Description: probably participates in ossification process
 C:Superfamily: osteoinductive factor precursor; leucine-rich alpha-2-glycoprotein repeat
 C:Keywords: glycoprotein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-322/Product: proteoglycan Lb #status predicted <WAT>
 F:145-167/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:168-191/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:192-211/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:212-237/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F:238-258/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F:259-282/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 F:283,302/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.5%; Score 249; DB 2; Length 322;
 Best Local Similarity 27.9%; Pred. No. 9.2e-10;
 Matches 77; Conservative 47; Mismatches 108; Indels 44; Gaps 9;
 Qy 41 DDDDDDDDDNSLFTPTREPRSHFFDLDL-----FPMCPFGCCQYSRVHCSDGLT 93
 Db 78 DNQEDKDEETPLRDLGSSQPEFFGLGPHTFNEFTCLL-CTCISTVTYVCDHEDL 136
 Qy 94 SVPTNPIDTRMLDQNNKKEIKENDFKGLTSLYGLILNANNKLTCKHKAFLTTKKLR 153
 Db 137 AIPP-LPKTTYFSRNRKINKNDPASFASLNDLKRIDLNSLISEDEDAFKLPHLQE 195
 Qy 154 LYLHNSQLSEIPLNPKSLAELRIHENKV--KKIQDTRFGMNAHVLMSANPLDNGGI 211
 Db 196 LVLKDNKIKQLP-ELPNTLTIDISNNRGRGKIGKQAEKDMYDLHLYITDNSLDH-- 251
 Qy 212 EPGAEGVTVFHRIAEAKLTSVPKGLPPTLLEHLDYNNKISIVLEDFKRYKELQRLGL 271
 Db 252 -----IPLPLFESRALHQLNNDILEMHEDTFCNKNLTYY-- 287
 Qy 272 GNNKITDIE-NGSLANTPRVREIHLNENKLIKIPSG 306
 Db 288 -KALEDIRLDCNINLSRTPQAYM---CLPRPIG 319

RESULT 34

A41915
 insulin-like growth factor-binding complex acid-labile chain precursor - human
 N:Alternate names: Acid-labile Subunit (ALS)
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999
 C:Accession: A41915
 R:Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.
 Mol. Endocrinol. 6, 870-876, 1992
 A:Title: Structure and functional expression of the acid-labile subunit of the insulin-like growth factor-binding complex
 A:Reference number: A41915; MUID:92357025; PMID:1379671
 A:Accession: A41915
 A:Status: preliminary
 A:Molecule type: mRNA; protein
 A:Residues: 1-605 <LEO>
 A:Cross-references: GB:M86826; NID:g184807; PIDN:AAA36047.1; PID:g184808

A:Experimental source: liver

A:Note: sequence extracted from NCBI backbone (NCBIP:110171)
 C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology
 F:75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F:171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F:195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 F:219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
 F:243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
 F:267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
 F:291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
 F:315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
 F:339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
 F:363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
 F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
 F:411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
 F:435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
 F:459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>
 F:483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>
 F:507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR19>

Query Match 12.3%; Score 246; DB 2; Length 605;

Best Local Similarity 25.3%; Pred. No. 3.4e-09;
 Matches 80; Conservative 61; Mismatches 133; Indels 42; Gaps 9;
 Qy 72 PMPFGCCQY-----SRVHCSDGLTTSVPTNPIDTRMLDQNNKKEIKENDFKGLT 125
 Db 39 PACPAACVCSYDDADELSVFCSSRNLTPLDPGPGGTQALWLDGNNLSSVPPAAFNLS 98
 Qy 126 SYGLTLNNKLTCKHKAFLTTKKLRILYLSHNSLSEIPLNL---PKSLAELRIHENKV 182
 Db 99 SLGLNLQGGQLGLEPQALLGLENLCHLHLERNQLRSALGTFAHTPALASGLSNRL 158
 Qy 183 KTKQDTRFGMNAHVLMSANPLDNGIEP-GAEGVTVFHRIAEAKLTSVPKGLPPT 241
 Db 159 SRLEGLFGLGSDMLNIGWNSL---AVLPDAAPRGL-----GS 195
 Qy 242 LLEHLDYNNKISIVLEDFKRYKELQRLGLGNKKTIDENGLANTPRVREIHLNENKLIK 301
 Db 196 LRELVLGNRLAYLPALPFGSLAELRELDLSRNALRAIKANVFQVLPRLQKLYLDRLNIA 255
 Qy 302 KI-PSGLPELKYLIQIFLHNSIARVGNVDFCTVPKMKKSLYSALSNPNPKTWEMQP 360
 Db 256 AVAPCAFLGLKALRWLDLSHNRVAGL-LEDTPPGLGLR-----VLRSLHNAIA--SLRP 307
 Qy 361 ATRFVLSRMSVOLGN 376
 Db 308 RTFKDLHFLLEELQLGH 323

RESULT 35

S42799
 gap precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jul-2000
 C:Accession: S42799; I37407
 R:Birnbaum, D.
 submitted to the EMBL Data Library, July 1993
 A:Reference number: S42799
 A:Accession: S42799
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-662 <BIR>
 R:Ollendorff, V.; Noguichi, T.; deLapeyriere, O.; Birnbaum, D.
 Cell Growth Differ. 5, 213-219, 1994
 A:Title: The GARP gene encodes a new member of the family of leucine-rich repeat-cont
 A:Reference number: I37407; MUID:94235567; PMID:8180135
 A:Accession: I37407
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-662 <RES>

A:Cross-references: EMBL:Z24680; NID:9439295; PIDN:CAA80847.1; PID:9439296

C:Genetics:

A:Gene: GDB:GARP; D11833F

A:Cross-references: GDB:433911

A:Map position: 11q13.5-11q14

C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology

F:50-73/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F:74-97/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F:98-121/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F:125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>

F:150-173/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

F:174-197/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

F:198-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

F:219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>

F:244-265/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>

F:266-289/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>

F:316-339/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>

F:340-363/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>

F:364-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>

F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>

F:411-433/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>

F:444-466/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>

F:467-490/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>

F:492-514/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>

F:515-536/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR19>

F:537-560/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR20>

Query Match 12.3%; Score 245; DB 2; Length 662;

Best Local Similarity 28.7%; Pred. No. 4.4e-09;

Matches 76; Conservative 47; Mismatches 104; Indels 38; Gaps 6;

QY 78 CQCYSRVHCDLGLTSVPTNIPFTRMLDQNNKIKEIKENDEKGLTSXYGLIINNKL 137

Db 26 KRWMDKVCQVLGLQVPSLPPTETLDLSGNQLRSILASPLGFTYALRHLDLSTNEI 85

QY 138 TKIHKAFITTKLRRLYLSHQLS-----EPL 166

Db 86 SFLOQFAQALTHLEHLSLAHNRKAMATALSAGGLGPLRVTSLDLSGNSLYSGLLERLL 145

QY 167 NLPLKSLAEIRIHNKVKIKQDTFGMNAHVLMSANPLDNGTEPCAFEGV-TVFHIR 225

Db 146 GEAPSLHTLSLAENSLTRITRTFRDMPALQDLHSNVLMD--IEDAFGLPRLTHIN 203

QY 226 IAEAKLTSVPKGLPTLELHLDYNNKISTVELEDFKRYK-ELQRLGLGNKKTIDENSL 284

Db 204 LSRNSLTICISDFSLQRLRLVLDSCNSIEAFQTASQAEFQTLWLDRENKLLHFPD--L 261

QY 285 ANIPRVRETHLENNKIKTPSLPE 309

Db 262 AALPRLIYLNLSNN-LIRLTPGPQ 285

RESULT 36

JC5239

insulin-like growth factor acid-labile chain - baboon

C:Species: Papio sp. (baboon)

C:Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997

C:Accession: JC5239

R:Delhanty, P.; Baxter, R.C.

Biochem. Biophys. Res. Commun. 227, 897-902, 1996

A:Title: The cloning and expression of the baboon acid-labile subunit of the insulin-like

A:Reference number: JC5239; MUID:97040714; PMID:8886027

A:Contents: liver

A:Accession: JC5239

A:Molecule type: mRNA

A:Residues: 1-605

C:Comment: This factor is structurally related to proinsulin and have insuline-like meta

Query Match

Best Local Similarity 12.1%; Score 241; DB 2; Length 605;

Matches 83; Conservative 59; Mismatches 132; Indels 42; Gaps 10;

QY 72 PMCPFGCQC-YSRVH-----CSDLGLTSVPTNIPFTRMLDQNNKIKEIKENDFKGLT 125

Db 39 PACATACACSDDEVNELSVFCSSRNLTTRPDGTPGQTALWLDNNLSIPPFAFNLS 98

QY 126 SLYGLIINNKLTKIHKPAFLTTTKLRRLYLSHNLSEIPLN---LPKSLAEIRIHNKV 182

Db 99 SLAFNLQGGSLGSLQALGLENLCHLHLRNQLSLAVGTFTPALALLGSLNNRL 158

QY 183 KKIQKDTFKGMNAHVLMSANPLDNGIEP-GAFEGVTVFHIRIAEAKLTSVPKGLPPT 241

Db 159 SRLEDGLFEGUGNLDNLGNLSL---AVLPDAARGL-----GG 195

QY 242 LLELHDYNNKISTVELEDFKRYKELQRLGLGNKKTIDENGLANIPRVREIHNKKLK 301

Db 196 LRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAKANVPAQLPRLQKLYLDRLNLA 255

QY 302 KI-PSGLPELKYLIIFLHNSIARVGNDFCTPVPKMKKSLYSALSIFNNPVKYMOP 360

Db 256 AVAFGAFGLKALRWLDLSHNRVAGL-LEDTFGLGLR-----VRLSHNAIA--SLRP 307

QY 361 ATFRVLSRMSVOLGN 376

Db 308 RTFEDLHFLBELQLCH 323

RESULT 37

JC4130

osteoglycin precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 20-Jun-2000

C:Accession: JC4130

R:Ujita, M.; Shinomura, T.; Kimata, K.

Gene 158, 237-240, 1995

A:Title: Molecular cloning of the mouse osteoglycin-encoding gene.

A:Reference number: JC4130; MUID:95331623; PMID:7607548

A:Accession: JC4130

A:Molecule type: mRNA

A:Residues: 1-298 <UJ>

A:Cross-references: DDBJ:D31951; NID:9971273; PIDN:BAA06721.1; PID:g1060928

C:Comment: This protein is a glycoprotein, belonging to the leucine-rich family. It i

C:Superfamily: osteoinductive factor precursor; leucine-rich alpha-2-glycoprotein rep

C:Keywords: chondroitin sulfate proteoglycan; glycoprotein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-298/Product: osteoglycin #status predicted <MAT>

F:129-254/Region: leucine-rich

F:144-167/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

F:101/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

F:258/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.8%; Score 235.5; DB 2; Length 298;

Best Local Similarity 26.3%; Pred. No. 6.9e-09;

Matches 89; Conservative 44; Mismatches 128; Indels 77; Gaps 11;

QY 4 YVLLFLALCSARPPFS-PSHI-----ALKNMMLKDMEDTDDDD 41

Db 8 FLLLFLVPLTQAQPSQSDLSHVNYEATGNSEETKFSQDYEDKYLDSIKETMIIP 67

QY 42 DDDDDDDDDNSLFTPREPSHFPPDLFPMCPFGCQCYSRVVHCDLGLTSVPTNIPF 101

Db 68 EKSLOKQKDEVIPSLPYKKEN-----DEMPTECLL-CVCLSGSVYCEEDIVAVPP-LPK 119

QY 102 DTRMLDQNNKIKEIKENDEKGLTSXYGLIINNKLTKIHKPAFLTTKLRRLYLSHNL 161

Db 120 ESAYLYARFNKIKKLTAKDFADMPNLRDLDTGNLIEDIEDGTFKSLSLLEELTAEENQL 179

QY 162 SEIPLNLPKSLAEIRIHNKVKK--IOKDTFGKMNALHVLMSANPLDNGIEPFAPEGV 219

Db 180 LRLPV-LPPKLTLLNAKHNKIKSGIKANTFKLNKLSFLY-----LDHNDLE----- 226

QY 220 TVFHIRIAEAKLTSVPKGLPTLELHLDYNNKISTVELEDFKRYKELQRLGLGNKKTID 279

Db 227 -----SVPNLPESLRVHILQFNSSISLTDFTCKANDTRYIR----- 264

QY 280 ENGLANIPRVREIHNK--KLKKIPSGLPKLYLQI 315

F; // -T00/D0main: leucine-rich alpha-2-glycoprotein repeat homolog <LRRL>

QY 166 LNLPKSLAE-----LRIHENKVKKIQKDTFRGMNAL 196

QY 166 LNLPKSLAE-----LRIHENKVKKIQKDTFRKGMNAL 196

Db 300 KGLLRLEQLLVLDLSCNQLTSHVDNSTFAGLRLVLNLSNALTRIGSKTFKELYFL 359
 QY 197 HVLEMSANPLDNNGIEPAGFEGTVFHIRIAEAKLTSVPKGLPPTLLEHLHDYKNKISTVE 256
 Db 360 QILDMRNSIGH--IEGAFPLPNLH-----TLNLAENRLHTLD 397
 QY 257 LEDFKRYKELQRLGLGNKTTDIENGSLANIPRVREIHLNENKLLKIPSGLPKYLQII 316
 Db 398 NRIFNGLYVLTKTLLNNLVSIVESAQAFRNCSDLKELDSSNQLTEVPEAVQDLSMLKTL 457
 QY 317 FLHNSIARVGVNDF 331
 Db 458 DLGENQISEFKNNTF 472

RESULT 41
 T13887
 tlr protein - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
 C:Accession: T13887
 R:Chiang, C.; Beachy, P.A.
 Mech. Dev. 47, 225-239, 1994
 A:Title: Expression of a novel Toll-like gene spans the parasegment boundary and contrib
 A:Reference number: Z17805; MUID:95151581; PMID:7848870
 A:Accession: T13887
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-1385 <CHI>
 A:Cross-references: EMBL:S76155; NID:g913247; PID:g913248; PIDN:AAB33383.1
 C:Genetics:
 A:Cross-references: FlyBase:Fbgn0004364
 A:Note: tlr

Query Match 11.2%; Score 223.5; DB 2; Length 1385;
 Best Local Similarity 25.9%; Pred. No. 3.4e-07;
 Matches 66; Conservative 42; Mismatches 96; Indels 51; Gaps 3;
 QY 106 LDLONNKIKEKDNDFKGLTSLYGLIINNKLTKIHPKAPLTKKKLRRLYLSNQLSEIP 165
 Db 240 LSLQHNNTIAPNALAGLSRLVNTSYNHLVSLPSEAFAGNKEURELHNGNDLYELP 299
 QY 166 LNLPKSLAE-----LRIHENKVKIKQDFTKGMNAL 196
 Db 300 KGLLRLEQLLVLDLSCNQLTSHVDNSTFAGLRLVLNLSNALTRIGSKTFKELYFL 359
 QY 197 HVLEMSANPLDNNGIEPAGFEGTVFHIRIAEAKLTSVPKGLPPTLLEHLHDYKNKISTVE 256
 Db 360 QILDMRNSIGH--IEGAFPLPNLH-----TLNLAENRLHTLD 397
 QY 257 LEDFKRYKELQRLGLGNKTTDIENGSLANIPRVREIHLNENKLLKIPSGLPKYLQII 316
 Db 398 NRIFNGLYVLTKTLLNNLVSIVESAQAFRNCSDLKELDSSNQLTEVPEAAQDLSMLKTL 457
 QY 317 FLHNSIARVGVNDF 331
 Db 458 DLGENQISEFKNNTF 472

RESULT 42
 T42998
 Ras-binding protein SUR-8 - Caenorhabditis elegans
 N:Alternate names: leucine-rich repeat protein
 C:Species: Caenorhabditis elegans
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
 C:Accession: T42998; T43192
 R:Selfors, L.M.; Schutzman, J.L.; Borland, C.Z.; Stern, M.J.
 Proc. Natl. Acad. Sci. U.S.A. 95, 6903-6908, 1998
 A:Title: Soc-2 encodes a leucine-rich repeat protein implicated in fibroblast growth fac
 A:Reference number: Z22280; MUID:98284030; PMID:9618511
 A:Accession: T42998
 A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA
 A:Residues: 1-559 <SEI>
 A:Cross-references: EMBL:AF054827; NID:g3293317; PIDN:AAC25697.1; PID:g3293318
 R:Sieburth, D.S.; Sun, Q.; Han, M.
 Cell 94, 119-130, 1998
 A:Title: SUR-8, a conserved Ras-binding protein with leucine-rich repeats, positively
 A:Reference number: Z22331; MUID:98337190; PMID:9674433
 A:Accession: T43192
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-559 <SIE>
 A:Cross-references: EMBL:AF068919; NID:g3252976; PIDN:AAC39129.1; PID:g3252977
 C:Genetics:
 A:Gene: soc-2

Query Match 11.2%; Score 223; DB 2; Length 559;
 Best Local Similarity 24.9%; Pred. No. 1.1e-07;
 Matches 84; Conservative 67; Mismatches 108; Indels 78; Gaps 14;
 QY 81 YSRVYHCSD-LGLTSVPTNIPFDTRMLDLQNNKIKEKENDPKGLTSLYGLIINNKLTK 139
 Db 174 YNRIYAVDEQIGNLS-----KLKMLDVRENKIRELPSAIGK-LTSLVWCLVSYNHLTR 225
 QY 140 IHPKAPLTKKKLRRLYLSNQLSEIPLNLPK--SLAELRIHENKVKIKQD----- 188
 Db 226 V-PEEIGDCHSLTQLDLQHNLSLPSYSGIKLVNLVRIGIRYNKIRCIPESELESCQOLEE 284
 QY 189 -----TFKGMNALHVLEMSANPL-----DNNGIEP-- 213
 Db 285 FIVESNHLQLLPPNLTMLPKIHTVNLRSNELTAFAPGQQFVSTVTINHEHNOISKIP 344
 QY 214 -GAFEGVT-VFHIRIAEAKLTSVP--KGLPPTLLEHLHDYKNKISTVELEDFKRYKELQRL 269
 Db 345 IGIFSKATRLTKLNKENELVSLPLDMGSWTSITELNSTNOLKVLPE-EDIEKLVNLEIL 403
 QY 270 GLGNKTTDIENGSLANIPRVREIHLNENKLLKIPSGLPKYLQIIIFLHNSI----- 323
 Db 404 VLSNNQKKLPN-QIGLNKRLDELDENELETVPTEIGFLOHLTKLWVQSNKILTPRS 462
 QY 324 -----ARGVNDPCTVPKMKKSLYSALSIFNN 351
 Db 463 IGNLCSLODLRLGNNL-TAIPETIGHLDSLKSLYLN 498

RESULT 43
 T23841
 hypothetical protein M88.6b - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T23841
 R:Sulston, J.
 submitted to the EMBL Data Library, June 1994
 A:Reference number: Z19806
 A:Accession: T23841
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-594 <WIL>
 A:Cross-references: EMBL:Z34802; PIDN:CAB54282.1; GSPDB:GN00021; CESP:M88.6b
 A:Experimental source: clone M88
 C:Genetics:
 A:Gene: CESP:M88.6b
 A:Map position: 3
 A:Introns: 40/3; 60/2; 101/3; 216/2; 290/1; 361/1; 411/3; 455/1; 544/3

Query Match 11.2%; Score 223; DB 2; Length 594;
 Best Local Similarity 26.1%; Pred. No. 1.2e-07;
 Matches 74; Conservative 59; Mismatches 109; Indels 42; Gaps 8;
 QY 59 REPRSHFFPDLFPMCPFCQCQYRVVHSDGLGTSVPTN-----IPFDTMLDLQNNKTK 114
 Db 87 ROSTVNVLPQDLFE-----NVFAKQVKLERCGLSLTQPNFSQSLGSAELLSRENRIK 140
 QY 115 EIKENDFKGLTSLYGLIINNKLTKIHPKAPLTKKKLRRLYLSHNSLSEIPLNL---PKS 171

Db 141 KLEKGLFTGLSKLTDLAMNKIQEIDVGAFAEELKKVEELLNENDIRVLTGTGTFDGMKN 200
Qy 172 LAELRIHENKVKKTKQDTFGKMAHVLMSANPLDNGNGIEGAFEGVTVFHIRIAEAKL 231
Db 201 LKLTQNCNLEIIOKGAFRGLNSLEQILISNNLEN--IDWTFISALK--NLRV----- 251
Qy 232 TSVPKGLPPTLLEHLHDYNNKISTVELEDKRYKELQRLGLGNNKITDIENGSLANIPRVR 291
Db 252 -----LDLGSNKISNVEMKSPFK---LEKLVNNTTIDSMKSIKLKDPLSLV 295
Qy 292 EIHLENNKKKIPS-----GLPELKYQLIIFLHNSIARVGVNDF 331
Db 296 VALFDRNKRKIESIGMDMDFGLTRSDRIETLSLARNLSQISPKAF 339
RESULT 44
T23836
hypothetical protein M88.6a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T23836
R:Sulston, J.
submitted to the EMBL Data Library, June 1994
A:Reference number: Z19806
A:Accession: T23836
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-610 <WTL>
A:Cross-references: EMBL:Z34802; PIDN:CAA84337.1; GSPDB:GN00021; CESP:M88.6a
A:Experimental source: clone M88
C:Genetics:
A:Gene: CESP:M88.6a
A:Map position: 3
A:Introns: 40/3; 60/2; 101/3; 216/2; 290/1; 427/3; 471/1; 560/3

Query Match 11.2%; Score 223; DB 2; Length 610;
Best Local Similarity 26.1%; Pred. No. 1.3e-07;
Matches 74; Conservative 59; Mismatches 109; Indels 42; Gaps 8;
Qy 59 REPRSHFFPDLPMCFPGQCQYSRVHVCSDLGLTSVPTN---IPFDTRMLDLONNKK 114
Db 87 RDSVTNVLPQDLFE-----NVFAKQVKLERCGLSLTLPNSFOSLGSRAELLSRENRIK 140
Qy 115 EIKENDFKGLTSLYGLILNNNKLTTHPKAFJTKKLRRLYLSHNLSEIPLNL---PKS 171
Db 141 KLEKGLFTGLSKLTDLAMNKIQEIDVGAFAEELKKVEELLNENDIRVLTGTGTFDGMKN 200
Qy 172 LAELRIHENKVKKTKQDTFGKMAHVLMSANPLDNGNGIEGAFEGVTVFHIRIAEAKL 231
Db 201 LKLTQNCNLEIIOKGAFRGLNSLEQILISNNLEN--IDWTFISALK--NLRV----- 251
Qy 232 TSVPKGLPPTLLEHLHDYNNKISTVELEDKRYKELQRLGLGNNKITDIENGSLANIPRVR 291
Db 252 -----LDLGSNKISNVEMKSPFK---LEKLVNNTTIDSMKSIKLKDPLSLV 295
Qy 292 EIHLENNKKKIPS-----GLPELKYQLIIFLHNSIARVGVNDF 331
Db 296 VALFDRNKRKIESIGMDMDFGLTRSDRIETLSLARNLSQISPKAF 339

RESULT 45
T30947
hypothetical protein AC7.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: T30947
R:Nelson, J.; Hawkins, J.
submitted to the EMBL Data Library, June 1999
A:Description: The sequence of C. elegans cosmid AC7.
A:Reference number: Z20944
A:Accession: T30947
A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA
A:Residues: 1-572 <NEL>
A:Cross-references: EMBL:U61957; PIDN:AA03417.2
A:Experimental source: strain Bristol N2; clone AC7
C:Genetics:
A:Map position: IV
A:Introns: 61/3; 105/3; 161/3; 234/1; 301/3; 375/1; 500/1
A:Note: AC7.2
Query Match 11.0%; Score 219; DB 2; Length 572;
Best Local Similarity 24.9%; Pred. No. 2.2e-07;
Matches 76; Conservative 65; Mismatches 100; Indels 64; Gaps 13;
Qy 81 YSRVVHVCSD-LGLTSVPTNIPFDTRMLDLONNKKIEKENDFKGLTSLYGLILNNNKLT 139
Db 179 YNRIYAVDEQIGNLS-----KKMLDVRENKIRELPSAIGK-LTSLVCLVSVNHLTR 230
Qy 140 IHPKAFJTKKLRRLYLSHNLSEIPLNLPK--SLAELRIHENKVKKIQKD----- 188
Db 231 V-PEEIGDCHSLTQDLQHNLSLPSYSGIKLVNLRIGIRYNKIRCIIPSESCQQL 289
Qy 189 -----TFKGMNALHVLMSANPL-----DNNGIEP-- 213
Db 290 FIVESNHLQLPPLNLTMLPKIHTVNLNSELTPAPPAGGPOQFVSTVTINNEHNOISKIP 349
Qy 214 -GAFEGVT-VFHIRIAEAKLTSPV--KGLPPTLLEHLHDYNNKISTVELEDKRYKELQRL 269
Db 350 IGIFSKATRLTKLNKENELVSLPLDMGWSWTSITELNSTQLKVLPE-EDIEKLVNLEIL 408
Qy 270 GLGNKKTIDDIENGSLANIPRVRHLENNKLLKPKSGLPPELKYLOITPLHNSIARV--G 327
Db 409 VLSNNQLKKLPN-QIGNLNKLRELDLENELETVTEIGFLQHLTKLWVQSNKILTLPRS 467
Qy 328 VDNDFC 332
Db 468 IGNLC 472
RESULT 46
A88684
protein AC7.2 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: A88684
R:anonymous, The C. elegans Sequencing Consortium.
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
Science 282, 2012-2018, 1998
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C-
A:Note: published errata appeared in Science 283, 55, 1999; Science 283, 2103, 1999;
A:Accession: A88684
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-613 <STO>
A:Cross-references: GB:chr_IV; PIDN:AA03418.1; PID:g1401355; GSPDB:GN00022; CESP:AC7
C:Genetics:
A:Map position: 4
Query Match 11.0%; Score 219; DB 2; Length 613;
Best Local Similarity 24.9%; Pred. No. 2.4e-07;
Matches 76; Conservative 65; Mismatches 100; Indels 64; Gaps 13;
Qy 81 YSRVVHVCSD-LGLTSVPTNIPFDTRMLDLONNKKIEKENDFKGLTSLYGLILNNNKLT 139
Db 220 YNRIYAVDEQIGNLS-----KKMLDVRENKIRELPSAIGK-LTSLVCLVSVNHLTR 271
Qy 140 IHPKAFJTKKLRRLYLSHNLSEIPLNLPK--SLAELRIHENKVKKIQKD----- 188
Db 272 V-PEEIGDCHSLTQDLQHNLSLPSYSGIKLVNLRIGIRYNKIRCIIPSESCQQL 330
Qy 189 -----TFKGMNALHVLMSANPL-----DNNGIEP-- 213

Db 172 -----VDLSNNSLTQILPGTLINLTNLTHLYLHNNKFTFIEQSF 212
Qy 309 ELKYLIQIFLHNS-----SIARVGVNDFCPTVPK 337
Db 213 QLLQLQETITLHNNRSCDHKONITYLLKWMYMETKAHVIGIPCSKQVSSLAKEQSMYPTPPG 272
Qy 338 MKKSIY-----SAISLFNNP-----VKYEMQPATFRCVLSR 369
Db 273 FTSSLFMTSEMGTVDITNSLSMVTQPKVTKPKOYRGKETTFGVTLSK 320
RESULT 49
Ad1822
leucine-rich-repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: Ad1822
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: Ad1822
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1119 <KUR>
A:Cross-references: GB:BA000019; PIDN:BAH77648.1; PID:gl17135102; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr0124

Query Match 10.9%; Score 216.5; DB 2; Length 1119;
Best Local Similarity 30.7%; Pred. No. 7.7e-07;
Matches 77; Conservative 47; Mismatches 94; Indels 33; Gaps 10;
Qy 92 LTSVP-----TNIPFTRMLDLQNNKKEIKENDFKGLTSLYGLIINNKKLTKIHPKAF 145
Db 161 ITEPEALAKUTNL-----TQNLNSYNQITEPEALAK-LTNLTQNLNRGNQRTETI-PEAL 214
Qy 146 LTTKRLRLYLSHNQSLSEIPLNLPK--SLAELRIHENKVKKIQDKTFKGMNALHVLMSA 203
Db 215 AKLTNLRLNSYNQRTETIPEALAKLNLQTLISLSDNQKEIPEITIAKLTNLTHLI-LSG 273
Qy 204 NPLDN-----NGIEPAGFVTVTHIRIAEAKLSVPGKLPPTLLEHLHDYNNKISTV 255
Db 274 NQKEIPEITIAKLTNLQTLGDLGNQKEIPEIAIAKLTN-----LTQLGLDGNQIKEI 325
Qy 256 ELEDPKRYKELQRLGLGNKKTIDTENGSLANIPRVREIHLNKKLKKIPSLPELKYLOI 315
Db 326 P-EATKLTNLTHLISLGNQKEIPE-TIAKLTNLQTLALSSNOITEIPEVLQTLNLQ 383
Qy 316 IFLHNSIARV 326
Db 384 LFLSSNQITQI 394

RESULT 50
S46224
peroxidase - fruit fly (Drosophila sp.)
C:Species: Drosophila sp.
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Oct-2000
C:Accession: S46224
R:Nelson, R.E.; Fessler, L.I.; Takagi, Y.; Blumberg, B.; Keene, D.R.; Olson, P.F.; Parke
EMBO J. 13, 3438-3447, 1994
A:Title: Peroxidase: a novel enzyme-matrix protein of Drosophila development.
A:Reference number: S46224; MUID:94341255; PMID:8062820
A:Accession: S46224
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1535 <NEL>
A:Cross-references: GB:U11052; NID:g531384; PIDN:AAA61568.1; PID:g531385
C:Superfamily: peroxidase; myeloperoxidase homology; proteoglycan amino-terminal homolo

F:19-44/Domain: proteoglycan amino-terminal homology <PAH4>
F:661-1350/Domain: myeloperoxidase homology <MPX>

Query Match 10.8%; Score 215.5; DB 2; Length 1535;
Best Local Similarity 32.5%; Pred. No. 1.4e-06;
Matches 55; Conservative 25; Mismatches 56; Indels 33; Gaps 4;

Qy 74 CPFGCOCYSRVVHCSDLGLTSVPTNIPEDTRMLDLQNNKKEIKENDFKGLTSLYGLILN 133
Db 26 CPAGCTCLERTVRCIRAKLSAVP-KLPQDTQTDLRFNHIEELPANAFSGLAQLTTLFLN 84
Qy 134 NNKLTIKIHPKAFITTKRLRLYLSHNQSLSEIPL----- 166
Db 85 DNELAYLDQALNGLTALRFVYLLNNNRLSRLPATIFQRMPLRLEGITFLENNDIWQLPAGLF 144
Qy 167 -NLPKSLAELRIHENKVKKIQDKTFKGMNALHVLMSANPLD---NNGI 211
Db 145 DNLPR-LNRLIMYNNKLTQLPYDGFENLNLNKLRLDGNNAIDIDCNCGV 192

Search completed: January 24, 2003, 12:27:32
Job time : 29 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 24, 2003, 12:21:30 ; Search time 14 Seconds
(without alignments)
1122.823 Million cell updates/sec

Title: US-09-944-457-2
Perfect score: 1992
Sequence: 1 MKEYVLLFLALCSAKPFPS.....PATFRCLVSRMSVQLGNFGM 379

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	1992	100.0	379	1	ASPN_HUMAN	Q9hxn1 homo sapien
2	1799	90.3	373	1	ASPN_MOUSE	Q99mq4 mus musculu
3	1044	52.4	368	1	PGS1_XENLA	Q91b75 xenopus lae
4	1040.5	52.2	369	1	PGS1_RAT	Q47853 rattus norv
5	1037.5	52.1	369	1	PGS1_MOUSE	Q28653 mus musculu
6	1034	51.9	368	1	PGS1_HUMAN	P21810 homo sapien
7	1028.5	51.6	372	1	PGS1_HORSE	O46403 equus cabal
8	1027.5	51.6	369	1	PGS1_SHEEP	O46390 ovis aries
9	1021.5	51.3	369	1	PGS1_CANFA	O02678 canis famil
10	1019.5	51.2	369	1	PGS1_BOVIN	P21809 bos taurus
11	974	48.9	356	1	PGS2_COTJA	Q9de68 coturnix co
12	969	48.6	357	1	PGS2_CHICK	P28675 gallus gall
13	967	48.5	360	1	PGS2_PIG	Q9xsd9 sus scrofa
14	963.5	48.4	359	1	PGS2_HUMAN	P07585 homo sapien
15	947	47.5	360	1	PGS2_SHEEP	Q9tte2 ovis aries
16	943	47.3	360	1	PGS2_BOVIN	P21793 bos taurus
17	941	47.2	360	1	PGS2_RABIT	Q28888 oryctolagus
18	939	47.1	360	1	PGS2_HORSE	O46542 equus cabal
19	934	46.9	360	1	PGS2_CANFA	Q29393 canis famil
20	907.5	45.6	354	1	PGS2_MOUSE	P28654 mus musculu
21	899	45.1	354	1	PGS2_RAT	Q01129 rattus norv
22	641	32.2	272	1	PGS1_PIG	Q9gkq6 sus scrofa
23	442	22.2	135	1	PGS1_RABIT	O46377 oryctolagus
24	399.5	20.1	343	1	LUM_CHICK	P51890 gallus gall
25	398.5	20.0	343	1	LUM_COTJA	Q9de67 coturnix co
26	390	19.6	338	1	LUM_HUMAN	P51884 homo sapien
27	384	19.3	342	1	LUM_BOVIN	Q05443 bos taurus
28	383	19.2	338	1	LUM_MOUSE	P51885 mus musculu
29	378	19.0	338	1	LUM_RAT	P51886 rattus norv
30	366	18.4	421	1	OMD_HUMAN	Q99983 homo sapien
31	363.5	18.2	646	1	FURL_HUMAN	Q9nzu0 homo sapien
32	361.5	18.1	381	1	PRLP_BOVIN	Q9gkn8 bos taurus
33	358.5	18.0	382	1	PRLP_HUMAN	P51888 homo sapien

ALIGNMENTS

RESULT 1

ASPN_HUMAN ID ASPN_HUMAN STANDARD: PRT; 379 AA.
AC Q9BXN1; Q96LD0; Q96K79;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Asporin precursor (Periodontal ligament associated protein-1) (PLAP-1).
DE 1).
GN ASPN OR PLAP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITE
ASN-281, MASS SPECTROMETRY, AND POLYMORPHISM OF POLY-ASP REGION.
RC TISSUE=Cartilage;
RX MEDLINE=21192276; PubMed=11152692;
RA Lorenzo P., Asperg A., Oennerfjord P., Bayliss M.T., Neame P.J.,
Heinegaard D.;
RT "Identification and characterization of asporin. A novel member of the
leucine-rich repeat protein family closely related to decorin and
biglycan.";
RL J. Biol. Chem. 276:12201-12211(2001).
RN [2]
RP SEQUENCE FROM N.A.
MEDLINE=21472263; PubMed=11587855;
RA Yamada S., Murakami S., Matoba R., Ozawa Y., Yokokoji T., Nakahira Y.,
Ikezawa K., Takayama S.-I., Matsubara K., Okada H.;
RT "Expression profile of active genes in human periodontal ligament and
isolation of PLAP-1, a novel SLRP family gene.";
RL Gene 275:279-286(2001).
RN [3]
RP SEQUENCE OF 1-242 FROM N.A.
RC TISSUE=Embryo;
RX Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RN Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RL [4]
RP PARTIAL SEQUENCE FROM N.A.
RX PubMed=11152695;
RA Henry S.P., Takanosu M., Boyd T.C., Mayne P.M., Eberspaecher H.,
Zhou W., de Crombrughe B., Hoeck M., Mayne R.;
RT "Expression pattern and gene characterization of asporin. A newly

34 356.5 17.9 377 1 PRLP_RAT
35 345 17.3 351 1 KERA_MOUSE
36 342.5 17.2 375 1 PMOD_BOVIN
37 342.5 17.2 378 1 PRLP_MOUSE
38 340.5 17.1 352 1 KERA_BOVIN
39 340.5 17.1 352 1 KERA_HUMAN
40 338 17.0 376 1 PMOD_RAT
41 338 17.0 422 1 OMD_BOVIN
42 333.5 16.7 380 1 PMOD_CHICK
43 331.5 16.6 649 1 FLR3_HUMAN
44 331 16.6 376 1 PMOD_MOUSE
45 325 16.3 353 1 KERA_CHICK
46 325 16.3 353 1 KERA_COTJA
47 325 16.3 376 1 PMOD_HUMAN
48 316 15.9 1480 1 SLIT_DROME
49 313.5 15.7 660 1 FLR2_HUMAN
50 306.5 15.4 423 1 OMD_MOUSE

O9eqp5 rattus norv
O35367 mus musculu
F13605 bos taurus
O9jk53 mus musculu
O62702 bos taurus
O60938 homo sapien
P50609 rattus norv
O77742 bos taurus
P51887 gallus gall
O9nzu0 homo sapien
P50608 mus musculu
O42235 gallus gall
O9de66 coturnix co
O60828 homo sapien
P24014 drosophila
O43155 homo sapien
O35103 mus musculu

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
 CC -!- TISSUE SPECIFICITY: Higher expression in heart, also detected in
 CC kidney, stomach, testes, and skin but only weakly in lung,
 CC skeletal muscle, small intestine, and thymus.
 CC -!- DEVELOPMENTAL STAGE: At 12.5 dpc, it is present in the mandibular
 CC as well as maxillary components of the first branchial arch. Also
 CC detected in the thoracic body wall adjacent to the heart. At 13.5
 CC dpc, it is detected in the mesenchyme lateral to Meckel's
 CC cartilage. Pronounced expression is observed in the perichondrium
 CC of the humerus, ribs, and scapula. At 14.5 dpc, it is detected in
 CC the mesenchymal condensations lateral to Meckel's cartilage, in
 CC the perichondrium surrounding the central cartilaginous elements
 CC of the vertebra and also in the dermal mesenchyme. At 15.5 dpc, it
 CC is expressed in the perichondrium/perioosteum of the long bones
 CC (i.e. femur, tibia, and fibula), some of the flat bones at the base
 CC of the skull (i.e. sphenoid bone), ribs, clavicle, and vertebrae.
 CC Also detected in the intramembranous bones of the maxilla and
 CC mandible (alveolar bone) and a strong expression is observed in
 CC sagittal sections of the subcutaneous muscles or panniculus
 CC carnosus of the thorax, trunk, and head/neck (platysma muscle)
 CC region. Very little expression is detected in the major
 CC parenchymal organs (with the exception of the large bronchi of the
 CC lung). Its expression is prominent in the developing mouse
 CC skeleton, particularly in the perichondrium/perioosteum of
 CC cartilage/bone, and is also found in other specialized connective
 CC tissues such as tendon, sclera, the connective tissue sheath
 CC surrounding muscle and dermis. In the sclera of the eye it is
 CC first detected at 15.5 dpc and stronger expression was detected at
 CC 17.5 dpc.
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
 CC (SLRPS) FAMILY. CLASS I SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
 CC -!- CAUTION: Ref.3 sequence differs from that shown due to a stop
 CC codon in position 238.

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 CC or send an email to license@isb-sib.ch).

DR EMBL; AF316825; AAK35162.1; -
 DR EMBL; AK014504; BAB29402.1; ALT_TERM.
 DR MGD; MGI:1913945; Aspn.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000372; LRR_Nterm.
 DR InterPro; IPR003592; LRR_out.
 DR InterPro; IPR003591; LRR_typ.
 DR Pfam; PF00560; LRR; 8.
 DR Pfam; PF01462; LRRNT; 1.
 DR SMART; SM00370; LRR; 3.
 DR SMART; SM00013; LRRNT; 1.
 DR SMART; SM00369; LRR_TYP; 7.
 KW Glycoprotein; Extracellular matrix; Signal; Repeat;
 FT SIGNAL 1 15 POTENTIAL.
 FT PROPEP 16 32 POTENTIAL.
 FT CHAIN 33 373 ASPORIN.
 FT DOMAIN 76 89
 FT REPEAT 89 109 CYS-RICH.
 FT REPEAT 110 133 LRR-S 1.
 FT REPEAT 134 157 LRR-T 1.
 FT REPEAT 158 178 LRR-T 2.
 FT REPEAT 179 202 LRR-S 2.
 FT REPEAT 203 227 LRR-T 3.
 FT REPEAT 203 227 LRR-T 4.

FT REPEAT 228 248 LRR-S 3.
 FT REPEAT 249 272 LRR-T 5.
 FT REPEAT 273 296 LRR-T 6.
 FT REPEAT 297 319 LRR-S 4.
 FT REPEAT 320 349 LRR-T 7.
 FT REPEAT 350 373 LRR-T 8.
 FT DOMAIN 36 45 POLY-ASP.
 FT DISULFID 326 359 BY SIMILARITY.
 FT CARBOHYD 48 48 O-LINKED (BY SIMILARITY).
 FT CARBOHYD 275 275 N-LINKED (GLNAC. . .) (POTENTIAL).
 SQ SEQUENCE 373 AA; 42572 MW; A50C4C82AABCF35 CRC64;
 Query Match 90.3%; Score 1799; DB 1; Length 373;
 Best Local Similarity 90.2%; Pred. No. 2.5e-117;
 Matches 34; Conservative 17; Mismatches 14; Indels 6; Gaps 1;
 QY 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDSLFPTR 60
 DB 1 MKEYVMLLLAVCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDSLFPTR 54
 QY 61 PRSHFFFDLPPMPCFCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEND 120
 DB 55 PVNFFFDLPPMPCFCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEND 114
 QY 121 FKGLTSLYGLTLNNKLTIKHPKAFLTTKLRLRLYLSHNSLSEPLNLPKSLAELRTHEN 180
 DB 115 FKGLTSLYALLNNKLTIKHPKFTLTTKLRLRLYLSHNSLSEPLNLPKSLAELRIHDN 174
 QY 181 KVKIKIQDTPFGMNAHVLEMSANPLDNGIEPAGFEGTVFHIRIAEAKLTSPVKGGLPP 240
 DB 175 KVKIKIQDTPFGMNAHVLEMSANPLDNGIEPAGFEGTVFHIRIAEAKLTSPVKGGLPP 234
 QY 241 TLELHLHDYKISTVELEDEKRYKELORLGLGNKKITDIENGSLANIPRVREIHLNKKL 300
 DB 235 TLELHLHDYKISTVELEDEKRYKELORLGLGNKKITDIENGSLANIPRVREIHLNKKL 294
 QY 301 KKIPSGPELKYLIQIFLHNSNARVGVNDFCTVPKMKKSLYSALSFNNPVKYWMQOP 360
 DB 295 KKIPSGQLKYLQIIFLHNSNARVGVNDFCTVPKMKKSLYSALSFNNPVKYWEIQP 354
 QY 361 ATFRCVLSRMSVQLGNFG 378
 DB 355 ATFRCVLSRMSVQLGNVG 372
 RESULT 3
 PGSL_XENLA
 ID PGSL_XENLA STANDARD; PRT; 368 AA.
 AC Q9IB75;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Bglican precursor.
 GN BGN.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 [1]
 RP SEQUENCE FROM N.A.
 RA Goto T., Kubota H.Y.;
 RT "cDNA of biglycan of Xenopus laevis.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May be involved in collagen fiber assembly (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
 CC (SLRPS) FAMILY. CLASS I SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
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CC -----
DR EMBL; AB037269; BAA90246.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_Out.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00560; LRR; 9.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00370; LRR; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_Typ; 1.
DR Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 368 BY SIMILARITY.
FT CHAIN 63 76 BIGLYCAN.
FT DOMAIN 82 102 CYS-RICH.
FT REPEAT 103 126 LRR-S 1.
FT REPEAT 127 150 LRR-T 1.
FT REPEAT 151 171 LRR-T 2.
FT REPEAT 172 195 LRR-S 2.
FT REPEAT 196 220 LRR-T 3.
FT REPEAT 221 241 LRR-T 4.
FT REPEAT 242 265 LRR-S 3.
FT REPEAT 266 289 LRR-T 5.
FT REPEAT 290 312 LRR-T 6.
FT REPEAT 313 342 LRR-T 7.
FT REPEAT 343 368 LRR-T 8.
FT DISULFID 63 76 BY SIMILARITY.
FT DISULFID 321 354 BY SIMILARITY.
SQ SEQUENCE 368 AA; 41197 MW; 53ADF7E7E3BDC528 CRC64;

Query Match 52.4%; Score 1044; DB 1; Length 368;
Best Local Similarity 58.1%; Pred. No. 3.3e-65;
Matches 193; Conservative 61; Mismatches 72; Indels 6; Gaps 3;

Qy 49 DQDNL--FPTRE-PRSHFPFDFLPPMPCGQCYSRVVCSDGLTSVPTNIPEDTRM 105
Db 38 DEASGVGPITESTIPDVGLPPMDL---CPFGCOHLRVVQCSDGLTSIPKPLPDFTTL 94
Qy 106 LDQNNKIKETKENDFKGLTSLYGLIINNKKLTKIHKAFLLTKKLRRLYLHSHQLSEIP 165
Db 95 LDQNNKITEIKDDFKGLTSLYGLIINNKKLTKIHKAFLLTKKLRRLYLHSHQLSEIP 154
Qy 166 LNLPLSLAELRIHENVKVKIKOKDTFKGMNALHVLMSANPLDNGLEPGAFGVTVFHIR 225
Db 155 KNLPLSLVELRIHENVKVKIKOKDTFKGMNALHVLMSANPLDNGLEPGAFGVTVFHIR 214
Qy 226 IAEAKLSVPKGLPPTLLEHLNKNKISTVELEDFKRYKELQRLGLGNKKITDENGSLA 285
Db 215 VSEAKLSGPKGLSTLNELHLDNNKLOAEKEDLSQASLYRLGLGNHNRIMENGSL 274
Qy 286 NIPRVREIHLNKKIKIPSGLPKLPKLYQIFLHNSIARVGVNDFCPTVPKMKKSLSYA 345
Db 275 FMPVRLHLDNNKLSRVPEGLPDMKLQVYVLSHNNITQGVNDFCPTVPKMKKSLSYA 334
Qy 346 ISLFNNPVKYMOPATFRVLSRMSVOLGNF 377
Db 335 ISLFNNPVYEVOPATFRVLSRMSVOLGNF 366

RESULT 4
PGS1_RAT
ID PGS1_RAT STANDARD; PRT; 369 AA.
AC P47853;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)
Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1).
BGN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RX SEQUENCE FROM N.A.
RC TISSUE=Vascular smooth muscle;
RX MEDLINE=91184222; PubMed=2081545;
RA Dreher K.L., Asundi V.K., Matzura D., Cowan K.;
RT "Vascular smooth muscle biglycan represents a highly conserved
RL proteoglycan within the arterial wall.";
RL Eur. J. Cell Biol. 53:296-304(1990).
CC -!- FUNCTION: May be involved in collagen fiber assembly (By
CC similarity).
CC -!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- TISSUE SPECIFICITY: Found in several connective tissues, specially
CC in articular cartilages.
CC -!- PTM: The two attached glycosaminoglycan chains can be either
CC chondroitin sulfate or dermatan sulfate (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SURPS) FAMILY. CLASS I SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).

```

EMBL: U17834; AAA58797.1; -.
 InterPro; IPR001611; LRR.
 InterPro; IPR000372; LRR_Nterm.
 InterPro; IPR003592; LRR_Out.
 InterPro; IPR003591; LRR_Typ.
 Pfam; PF00560; LRR; 8.
 Pfam; PF01462; LRRNT; 1.
 SMART; SM00370; LRR; 3.
 SMART; SM00013; LRRNT; 1.
 SMART; SM00369; LRR_Typ; 1.
 Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 Leucine-rich repeat; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT PROPEP 20 37
 FT CHAIN 38 369
 FT DOMAIN 64 77
 FT REPEAT 83 103
 FT REPEAT 104 127
 FT REPEAT 128 151
 FT REPEAT 152 172
 FT REPEAT 173 196
 FT REPEAT 197 221
 FT REPEAT 222 242
 FT REPEAT 243 266
 FT REPEAT 267 290
 FT REPEAT 291 313
 FT REPEAT 314 343
 FT REPEAT 344 369
 FT CARBOHYD 42 42
 FT CARBOHYD 48 48
 FT CARBOHYD 271 271
 FT CARBOHYD 312 312
 FT DISULFID 64 77
 FT DISULFID 322 355
 FT DISULFID 369 AA; 41706 MW; 319DC15117F2C604 CRC64;
 SEQUENCE

DR	EMBL; X53928; CAA37875.1; -
DR	EMBL; L20276; AAA64360.1; -
DR	EMBL; BC005452; AAH05452.1; -
DR	EMBL; BC019502; AAH19502.1; -
DR	EMBL; Y11758; CAA72422.1; -
DR	PIR; S20811; S20811.
DR	MGD; MGI:88158; Bgn.
DR	InterPro; IPR001611; LRR.
DR	InterPro; IPR000372; LRR_Nterm.
DR	InterPro; IPR003592; LRR_out.
DR	InterPro; IPR003591; LRR_type.
DR	Pfam; PF00560; LRR; 8.
DR	Pfam; PF01462; LRRNT.1.

		SIGNAL	1 19	POTENTIAL.	
SMART;	SMO0370; LRR- 3.	LFT PROPEP	20 37		
DR SMART;	SMO0013; LRRNT; 1.	FTH CHAIN	38 369	BIGLYCAN.	
DDR SMART;	SMO0369; LRR_TYP; 1.	FTH DOMAIN	64 77	CYS-RICH.	
KK Glycoprotein; Extracellular		FTH REPEAT	83 103	LRR-S 1.	
Leucine-rich repeat; Signal.		FTH REPEAT	104 127	LRR-T 1.	
		FTH REPEAT	128 151	LRR-T 2.	
		FTH REPEAT	152 172	LRR-S 2.	
		FTH REPEAT	173 196	LRR-T 3.	
		FTH REPEAT	197 221	LRR-T 4.	
		FTH REPEAT	222 242	LRR-S 3.	
		FTH REPEAT	243 266	LRR-T 5.	
		FTH REPEAT	267 290	LRR-T 6.	
		FTH REPEAT	291 313	LRR-S 4.	
		FTH REPEAT	314 343	LRR-T 7.	
		FTH REPEAT	344 369	LRR-T 8.	
		CARBOHYD	42 42	O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY).	(BY
		FTH CARBOHYD	48 48	O-LINKED (GLYCOSAMINOGLYCAN)	(BY
		FTH CARBOHYD	271 271	N-LINKED (GLCNAC. .) (POTENTIAL).	.
		FTH CARBOHYD	312 312	N-LINKED (GLCNAC. .) (POTENTIAL).	.
		FTH DISULFID	64 77	BY SIMILARITY.	
		FTH DISULFID	322 355	BY SIMILARITY.	
		FTH CONFLICT	68 68	C -> W (IN REF. 2).	
		FTH SEQUENCE	369 AA; 4163 MW;	CMC 4B57FC9A1026BE6 CRC64;	
		SQL			

QY 60 EPRSHFPFDFPMCPGOCYGRVYHCSDLGLTSVPTNIPFTRMLDQNNKIKEIKEN 119
 Db 60 -----FSAMCPGCHLRVQCSDGLGKTVPKETSPPTLLDQNNKISLRKD 109
 QY 120 DFGLTSLYGLILNNKTKIHPKAFATTKKRLRLYLSHNOJSEIPLNLPKSLAEIURIHE 179
 Db 110 DFGLQHLVYALVNNKISKIHEKATSPRLKQLKLYSKNHLVEIPNLPSSLSVLRHID 169
 QY 180 NKVKIKOQDFKGMNALHVLMSANPLDNNCIEPGAEGVTVPHIRIAEAKLTSVPKGLP 239
 Db 170 NRIRKVPKGVSGLRNNNCIEMGNPLENSGFEPGAFDGLKLYLRISAKLTGIPKDL 229
 QY 240 PTLLEHLDYKSTVELEDFKRYKELQRLGLGNKTKITDIENGLANIPRVRIHLNNK 299
 Db 230 ETLNELHLDHKNKIOAIELEDLRLYSKLYRLGLGHNOIRMTENGSLSLFPLTLRELHLDNNK 289
 QY 300 LKTPSGLPKLYLQIIFLHNSNITARVGVNDPCTVPKMKKSLYSALSANNPVKWEQ 359
 Db 290 LSRVPAGLPDLKLVVYLSHNNITKVGINDFCMPGFGVKRAYINGISLFNNPVPYWEQ 349
 QY 360 PATFRCVLSRMSVOLGNF 377
 Db 350 PATFRCVTDRLAIOFGNY 367

RESULT 6
 PGSL_HUMAN STANDARD; PRT; 368 AA.
 AC P21810; P13247;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1).
 GN BGN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone;
 RX MEDLINE=89174714; PubMed=2647739;
 RA Fisher L.W., Termine J.D., Young M.F.;
 RT "Deduced protein sequence of bone small proteoglycan I (biglycan)
 RT shows homology with proteoglycan II (decorin) and several
 RT nonconnective tissue proteins in a variety of species.";
 RL J. Biol. Chem. 264:4571-4576(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91317791; PubMed=1860845;
 RA Fisher L.W., Heegaard A.M., Vetter U., Vogel W., Just W.,
 RA Termine J.D., Young M.F.;
 RT "Human biglycan gene. Putative promoter, intron-exon junctions, and
 RT chromosomal localization.";
 RL J. Biol. Chem. 266:14371-14377(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20314869; PubMed=10854409;
 RA Mallon A.M., Platzer M., Bates R., Gloeckner G., Botcherby M.,
 RA Nordsiek G., Strivens M.A., Kioschis P., Dangel A., Cunningham D.,
 RA Straw R., Weston P., Hunter C., Gilbert M., Fernando S., Goodall K.,
 RA Kerry G., Greystrom J.S., Clark D., Goerdes M., Blechschmidt K.,
 RA Rump A., Hinzmann B., Mundy C.R., Miller W., Poustka A., Herman G.E.,
 RA Rhodes M., Denny P., Rosenthal A., Brown S.D.M.;
 RT "Comparative genome sequence analysis of the Bpa/Str region in mouse
 RT and man.";
 RL Genome Res. 10:758-775(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]

RP SEQUENCE OF 38-57.
 RX MEDLINE=90073579; PubMed=2590169;
 RA Roughley P.J., White R.J.;
 RT "Dermatan sulphate proteoglycans of human articular cartilage. The
 RT properties of dermatan sulphate proteoglycans I and II.";
 RL Biochem. J. 262:823-827(1989).
 RN [6]
 RP SEQUENCE OF 38-66.
 RX MEDLINE=87250639; PubMed=3597437;
 RA Fisher L.W., Hawkins G.R., Termine J.D.;
 RT "Purification and partial characterization of small proteoglycans I
 RT and II, bone sialoproteins I and II, and osteonectin from the mineral
 RT compartment of developing human bone.";
 RL J. Biol. Chem. 262:9702-9708(1987).
 RN [7]
 RP SEQUENCE OF 361-368 FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=95187185; PubMed=7881444;
 RA Just W., Rau W., Muller R., Geerrens C., Vogel W.;
 RT "Dinucleotide repeat polymorphism at the human biglycan (BGN)
 RT locus.";
 RL Hum. Mol. Genet. 3:2268-2268(1994).
 CC -!- FUNCTION: May be involved in collagen fiber assembly (By
 CC similarity).
 CC -!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
 CC -!- TISSUE SPECIFICITY: Found in several connective tissues, specially
 CC in articular cartilages.
 CC -!- PTM: The two attached glycosaminoglycan chains can be either
 CC chondroitin sulfate or dermatan sulfate (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
 CC (SLRPS) FAMILY. CLASS I SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; J04599; AAA36009.1; -;
 CC EMBL; M65153; AAA52287.1; ALT_SEQ.
 CC EMBL; M65152; AAA52287.1; JOINED.
 CC EMBL; U82695; AAF33530.1; -;
 CC EMBL; BC002416; AAH02416.1; -;
 CC EMBL; BC004244; AAH04244.1; -;
 CC EMBL; U11686; AAC50117.1; -;
 CC PIR; A28457; A28457.
 CC PIR; A32458; A32458.
 CC PIR; A40757; A40757.
 CC PIR; S05639; S05639.
 CC Genew; HGNC:1044; BGN.
 CC MIM; 301870; -;
 CC InterPro; IPR001611; LRR.
 CC InterPro; IPR000372; LRR_Nterm.
 CC InterPro; IPR003592; LRR_out.
 CC InterPro; IPR003591; LRR_type.
 CC Pfam; PF00560; LRR; 8.
 CC Pfam; PF01462; LRRNT; 1.
 CC SMART; SM00370; LRR; 3.
 CC SMART; SM00013; LRRNT; 1.
 CC SMART; SM00369; LRR_TYP; 1.
 CC Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 KW Leucine-rich repeat; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT PROPEP 20 37
 FT CHAIN 38 368 BIGLYCAN.
 FT DOMAIN 63 76 CYS-RICH.
 FT REPEAT 82 102 LRR-S 1.
 FT REPEAT 103 126 LRR-T 1.

FT REPEAT 127 150 LRR-T 2.
 FT REPEAT 151 171 LRR-S 2.
 FT REPEAT 172 195 LRR-T 3.
 FT REPEAT 196 220 LRR-T 4.
 FT REPEAT 221 241 LRR-S 3.
 FT REPEAT 242 265 LRR-T 5.
 FT REPEAT 266 289 LRR-T 6.
 FT REPEAT 290 312 LRR-S 4.
 FT REPEAT 313 342 LRR-T 7.
 FT REPEAT 343 368 LRR-T 8.
 FT CARBOHYD 42 42 O-LINKED (GLYCOSAMINOGLYCAN).
 FT CARBOHYD 47 47 N-LINKED (GLYCOSAMINOGLYCAN).
 FT CARBOHYD 270 270 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 311 311 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT DISULFID 63 76 BY SIMILARITY.
 FT DISULFID 321 354 BY SIMILARITY.
 FT CONFLICT 139 140 KL -> NV (IN REF. 1).
 FT CONFLICT 163 164 EL -> DV (IN REF. 1).
 SQ SEQUENCE 368 AA; 41654 MW; BF16F304C5CD3B3E CRC64;

Query Match 51.9%; Score 1034; DB 1; Length 368;
 Best Local Similarity 53.2%; Pred. No. 1.6e-64;
 Matches 200; Conservative 63; Mismatches 93; Indels 20; Gaps 3;

QY 6 LLLFLALCSAKPF----FSPSHIALKNMMLKDMEDTDDDDDDDDDDDDSDNSLFPPTREP 61
 Db 7 LVSLALLSQALPFEQGFWDFTLDDGPPMNDDEASGADTSGVLDPD-----SVTPYIS- 60

QY 62 RSHFFPDLFPMCPFGCOCYSRVVHCSDGLTSGTVPNTIPFTRMLDLQNNKIRKENDF 121
 Db 61 -----AMCPFGCHLRVQCSDLGLKSPKESIPDPTTLLDQNNIDSELKDDF 110

QY 122 KGLTSLYGLIINNKKLTHPKAFLLTKKRLRYLSHNSLSEIPLNPKSLAEIRIHENK 181
 Db 111 KGLHLYALVNNKISKIHEKAFSPRLKQKLYISKNHVEIPNPLSSLVEIRIHDRN 170

QY 182 VKKIQKDTFGKGNALHVLMSANPLDNGIEPGAFEGVTFHIRIARAKLTSPKGLPPT 241
 Db 171 IRKVPKGVGLRNMCNTEGNGNPLESGEPGAFDGLKLYLRISAKLTGPKDLPET 230

QY 242 LLEHLIDYKNTSTVEDEFKYKELQRLGLGNKNTIDENGSLANIPRVREIHLNKKLK 301
 Db 231 LNEHLIDHNTQALEDELLRYKLYRLGLGHQIRMIENGSLFSLPTLRELHLDNNKLA 290

QY 302 KIPSLPELKYLIQIFILHSNIARVGNDVCPVTPKPKSKLYSAISLFNNPVKYEWOQA 361
 Db 291 RVPSSLPDLKLLQVYLLHNNITKVGNDVCPMGFGYKRAYNYNGISLFNNPVKYEWOQA 350

QY 362 TFRCLVSRMSVOLGNF 377
 Db 351 TFRCLVSRMSVOLGNF 366

RESULT 7

PGSI_HORSE STANDARD; PRT; 372 AA.
 AC 04603; Q9NIU5;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1).
 GN BGN.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Richardson D.W., Dodge G.R.;
 RT "Dose dependent effects of corticosteroids on the expression of matrix
 related genes in equine articular chondrocytes";
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE OF 150-192 FROM N.A.
 RX MEDLINE=20082971; PubMed=10613847;
 RA Caetano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
 RA Bowling A.T., Murray J.D.;
 RT "A comparative gene map of the horse (Equus caballus).";
 RL Genome Res. 9:1239-1249(1999).
 CC -!- FUNCTION: May be involved in collagen fiber assembly (By
 CC similarity).
 CC -!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
 CC -!- PTM: The two attached glycosaminoglycan chains can be either
 CC chondroitin sulfate or dermatan sulfate (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
 CC (SLRPS) FAMILY. CLASS 1 SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; AF035934; AAB89305.1; -;
 DR EMBL; AF135020; AAF64248.1; -;
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000372; LRR_Nterm.
 DR InterPro: IPR003592; LRR_out.
 DR InterPro: IPR003591; LRR_typ.
 DR Pfam: PF00560; LRR; 7.
 DR Pfam: PF01462; LRRNT; 1.
 DR SMART; SM00370; LRR; 3.
 DR SMART; SM00013; LRRNT; 1.
 DR SMART; SM00369; LRR_TYP; 1.
 DR KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 KW Leucine-rich repeat; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT PROPEP 23 40 BY SIMILARITY.
 FT CHAIN 41 372 BIGLYCAN.
 FT DOMAIN 67 80 CYS-RICH.
 FT REPEAT 86 106 LRR-S 1.
 FT REPEAT 107 130 LRR-T 1.
 FT REPEAT 131 154 LRR-T 2.
 FT REPEAT 155 175 LRR-S 2.
 FT REPEAT 176 199 LRR-T 3.
 FT REPEAT 200 224 LRR-T 4.
 FT REPEAT 225 245 LRR-S 3.
 FT REPEAT 246 269 LRR-T 5.
 FT REPEAT 270 293 LRR-T 6.
 FT REPEAT 294 316 LRR-S 4.
 FT REPEAT 317 346 LRR-T 7.
 FT REPEAT 347 372 LRR-T 8.
 FT CARBOHYD 45 45 O-LINKED (GLYCOSAMINOGLYCAN) (BY
 FT SIMILARITY).
 FT CARBOHYD 51 51 O-LINKED (GLYCOSAMINOGLYCAN) (BY
 FT SIMILARITY).
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT DISULFID 67 80 BY SIMILARITY.
 FT DISULFID 325 358 BY SIMILARITY.
 SQ SEQUENCE 372 AA; 41924 MW; D0BBF8576C5F082E CRC64;

Query Match 51.6%; Score 1028.5; DB 1; Length 372;
 Best Local Similarity 52.4%; Pred. No. 3.9e-64;
 Matches 198; Conservative 67; Mismatches 94; Indels 19; Gaps 3;

QY 4 YVLLFLALCSAKPF----FSPSHIALKNMMLKDMEDTDDDDDDDDDDSDNSLFPPT 59
 Db 8 WLIALSLLSQALPFEQGFWDFTLDDGPPMNDDEASGADTSGIPDJD-----SLTPP- 62

QY 60 EPRSHFFPDLFPMCPFGCOCYSRVVHCSDGLTSGTVPNTIPFTRMLDLQNNKIRK 119

54 DALTPPTYS----AMCPFGCHLRVVOQCSDLGLKAVPKEISPDTMLIDLQNNDISELRAD 109
 QY 120 DFKGLTSLYGLIINNNKLTITHPKAFLTTKKLRLLYSLHNQOLSEIPLNLPKSLAELRIHE 179
 Db 110 DFKGLHHLYALVLNNKISIKIHEKAFSPLRKLOKLYISKNHLVEIPNPSSLVELRIHD 169
 QY 180 NKVKIKQDFTKGMNALHVLSEMSANPLDNNNGIEPGAFEGVTVPFHRIAETKLTSPVKGLP 239
 Db 170 NRIRKVPKGVFSGLRNNMCIEGMGNPLENSGFEFGADGLKLNLYLRSEAKLTGIPKDL 229
 QY 240 PTLELHDYNKISTVELEDFKRYKELQRLGLGNKKITDIENGLANIPKVRHLENKK 299
 Db 230 ETLELHDHNKIQAIETEDLLRYSKLYRLGLGHQNRMTIENGSLSFPLPTRELHLDNNK 289
 QY 300 LKTIPLGLPELKLYQIIFLHNSIARVGNDFCPTVPKVKKSLYSALSLFNPNPKYWEQ 359
 Db 290 LSRVPSGLPKLQVYLHNTNITKVGNDFCVPGFVGKRAYINGISLUFNNPVPYWEVO 349
 QY 360 PATFRCVLSRMSYQLGNF 377
 Db 350 PATFRCVTDRLAIQFGNY 367

 RESULT 10
 PGSL_BOVIN STANDARD; PRT; 369 AA.
 ID AC PGSL_BOVIN STANDARD; PRT; 369 AA.
 AD P21809; P79259;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1) (leucine-rich PG I).
 DE DE
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aorta;
 RX MEDLINE=96113563; PubMed=86730009;
 RA Xu J.H., Radhakrishnamurthy B., Srinivasan S.R., Berenson G.S.;
 RT "Primary structure of bovine aorta biglycan core protein deduced from
 RL cloned cDNA.";
 RL Biochem. Mol. Biol. Int. 37:263-272(1995).
 RN [2]
 RP SEQUENCE OF 38-63.
 RC TISSUE=Cartilage;
 RX MEDLINE=8925324; PubMed=2656687;
 RA Neame P.J., Choi H.U., Rosenberg L.C.;
 RT "The primary structure of the core protein of the small, leucine-rich
 RL proteoglycan (PG I) from bovine articular cartilage.";
 RL J. Biol. Chem. 264:8653-8661(1989).
 RN [3]
 RP SEQUENCE OF 38-63.
 RC TISSUE=Cartilage;
 RX MEDLINE=89123388; PubMed=2914936;
 RA Choi H.U., Johnson T.L., Pal S., Tang L.H., Rosenberg L.C.,
 RA Neame P.J.;
 RT "Characterization of the dermatan sulfate proteoglycans, DS-PGI and
 RL DS-PGII, from bovine articular cartilage and skin isolated by octyl-
 RT sepharose chromatography.";
 RL J. Biol. Chem. 264:2876-2884(1989).
 RN [4]
 RP INTERACTIONS WITH MFAP2 AND ELN.
 RX PubMed=11723132;
 RA Reinboth B., Hanssen E., Cleary E.G., Gibson M.A.;
 RT "Molecular interactions of biglycan and decorin with elastic fiber
 RL components: biglycan forms a ternary complex with tropoelastin and
 RT microfibril-associated glycoprotein 1.";
 RL J. Biol. Chem. 277:3950-3957(2002).
 RC !- FUNCTION: May be involved in collagen fiber assembly.


```

QY 65 FFPEDLPMPGFCQCYSRVHVCSDGLTGVPTNIPDTRMLDLQNNKIKETKENDFKGL 124
Db 47 TGF-----PVCPRCQCHLRVQVQCDGLERVPKDLDPDPTLLDLQNNKIKETKENDFKGL 102
QY 125 TSLYGLIINNKKLTIKHPKAFITTKLRLRLYLSHNQLSEIPLNPKSLAELRIHENKVK 184
Db 103 KNLHALIVNNKISKISPAAPAPLKKLERLYLSKNKIKELPENPKSLQIRAHENEISK 162
QY 185 IOKDTFKGNALHYLEMSANPLDNGTEPCAFEGV-TVFHIRIAEAKLTSPVKGLPPTLL 243
Db 163 LRKAVFNGLVNOIVLEGTNPLKSSGLENGAFQGMKLSYIRIADNTITSIPKGLPPLT 222
QY 244 ELHDYNNKISTVELEDFKRYKELQRLGLGNKKTIDIEGSLANIPRVREIHLNENKIKKI 303
Db 223 ELHDGNKISDAEGLSGLTNLAKLGLSPNSISSEVSGSLNVPVPHLRELHLNNELVRV 282
QY 304 PSGLPPELKYLIQIIFLHNSIARVGVNDFCPTVPKMKSLYSALSLENPNPKYKHEMOPATF 363
Db 283 PSGLGEHKYIQVYVYHLNKKIASIGINDFCPLGYNTKATYSVGLSFSPNPVQYWEIQPSAF 342
QY 364 RCVLSRMSVOLGNF 377
Db 343 RCIHERSAVQIGNY 356

RESULT 13
PGS2_PIG
ID PGS2_PIG STANDARD; PRT; 360 AA.
AC OXSD9: O9XSH4;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (PG-S2).
GN DCN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RN SEQUENCE FROM N.A. (LONG ISOFORM).
RC STRAIN=Yorkshire;
RA Stephenson S., Schnoke M., Vesely I.;
RT "Cloning of the porcine decorin gene.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A. (SHORT ISOFORM).
RC STRAIN=Yorkshire; TISSUE=Aorta;
RA Stephenson S., Schnoke M., Vesely I.;
RT "Alternatively spliced version of the porcine decorin gene.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May affect the rate of fibrils formation (By
CC similarity).
CC -!- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here)
CC and a short form; are produced by alternative splicing.
CC -!- PM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
CC (SRPS) FAMILY. CLASS I SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC -----
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DR EMBL; AF125537; AAD23578.1; -.
DR EMBL; AF140270; AAD33862.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_type.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00370; LRR; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_TYP; 2.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal; Alternative splicing.
FT SIGNAL 16
FT PROPEP 17 30
FT CHAIN 31 360
FT DOMAIN 55 68
FT REPEAT 74 94
FT REPEAT 95 118
FT REPEAT 119 142
FT REPEAT 143 163
FT REPEAT 164 187
FT REPEAT 188 213
FT REPEAT 214 234
FT REPEAT 235 258
FT REPEAT 259 282
FT REPEAT 283 305
FT REPEAT 306 335
FT REPEAT 336 360
FT DISULFID 55 68
FT DISULFID 314 347
FT CARBOHYD 34 34
FT CARBOHYD 212 212
FT CARBOHYD 263 263
FT CARBOHYD 304 304
FT VARSPLIC 281 318
FT VARSPLIC 360 AA; 39899 MW; 8573DE8DDEBA7509 CRC64;
SQ
Query Match 48.5%; Score 967; DB 1; Length 360;
Best Local Similarity 50.9%; Pred. No. 6.6e-60;
Matches 193; Conservative 63; Mismatches 101; Indels 22; Gaps 5;
QY 1 MKEYVLLLFALCS-AKPFPSHTALKMKMEDTDDDDDDDDDDDDDDDDDDDDDDSLFPTR 59
Db 1 MKATIVFLLLAQVSWAGPF---QQKGLDFMLEDEASIGEDREPE-----VPEL 48
QY 60 EPRSHFFPFDLPMPGFCQCYSRVHVCSDGLTGVPTNIPDTRMLDLQNNKIKETK 119
Db 49 EP-----LGPMCPFCQCHLRVQVQCDGLDKVVKDLPPDPTALLDLQNNKITEIKDG 100
QY 120 DPKGLTSLYGLIINNKKLTIKHPKAFITTKLRLRLYLSHNQLSEIPLNPKSLAELRIHE 179
Db 101 DPKNLKLNHTLLIINNKKISKISPGAFAPLVKLERLYLSKNKIKELPENPKTLQELRYHE 160
QY 180 NKVKIKOKDTFKGNALHYLEMSANPLDNGTEPCAFEGV-TVFHIRIAEAKLTSPVKGL 238
Db 161 NEITVRKAVFNGLVNOIVLEGTNPLKSSGLENGAFQGMKLSYIRIADNTITSIPGL 220
QY 239 PPTLLEHLHDYNNKISTVELEDFKRYKELQRLGLGNKKTIDIEGSLANIPRVREIHLNEN 298
Db 221 PPSLTDELHDGNKISKVDAASLKLNNLAKLGLGFNSISTVDGSLANTPHLRELHLNEN 280
QY 299 KKKKIPSGLPPELKYLIQIIFLHNSIARVGVNDFCPTVPKMKSLYSALSLENPNPKYKHEM 358
Db 281 KLNKVPGGIAEHKYIQVYVYHLNKKIASIGINDFCPLGYNTKATYSVGLSFSPNPVQYWEI 340
QY 359 QPATERCVLSRMSVOLGNF 377
Db 341 QPSTFCVYVRSALQIGNY 359

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RESULT 14

PGS2_HUMAN
ID PGS2_HUMAN STANDARD; PRT: 359 AA.
AC P07585; Q9Y5N9; Q9P0Z0; Q9P0Z1;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (PG-S2) (PG40).
GN DCN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN MEDLINE=87017013; PubMed=3484330;
RA Krusius T., Ruoslahti E.;
RP "Primary structure of an extracellular matrix proteoglycan core
RT protein deduced from cloned cDNA";
RL Proc. Natl. Acad. Sci. U.S.A. 83:7683-7687(1986).
[2]
RN MEDLINE=93162643; PubMed=8432527;
RA Vetter U., Vogel W., Just W., Young M.F., Fisher L.W.;
RP "Human decorin gene: Intron-exon junctions and chromosomal
RT localization";
RL Genomics 15:161-168(1993).
[3]
RN MEDLINE=93162642; PubMed=8432526;
RA Danielson K.G., Fazio A., Cohen I.R., Cannizzaro L., Iozzo R.V.;
RP "The human decorin gene: Intron-exon organization, discovery of two
RT alternatively spliced exons in the 5' untranslated region, and
RL mapping of the gene to chromosome 12q23.";
RN Genomics 15:146-160(1993).
[4]
RN MEDLINE=87250639; PubMed=3597437;
RA Fisher L.W., Hawkins G.R., Termine J.D.;
RP "Purification and partial characterization of small proteoglycans I
RT and II, bone sialoproteins I and II, and osteonectin from the mineral
RL compartment of developing human bone.";
RN J. Biol. Chem. 262:9702-9708(1987).
CC -!- FUNCTION: May affect the rate of fibrils formation.
CC -!- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (by
CC similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS: 5 isoforms; A (shown here), B, C, D and E;
CC are produced by alternative splicing.
CC -!- PM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin.
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
CC (SLRPS) FAMILY, CLASS I SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).

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CC EMBL: M14219; AA000774.1; -
DR EMBL: L01131; AAA52301.1; ALT_SEQ.
DR EMBL: L01125; AAA52301.1; JOINED.
DR EMBL: L01126; AAA52301.1; JOINED.
DR EMBL: L01127; AAA52301.1; JOINED.
DR EMBL: L01129; AAA52301.1; JOINED.
DR EMBL: L01130; AAA52301.1; JOINED.
DR EMBL: M98262; AAB60901.1; -
DR EMBL: AF138300; AAD4713.1; -
DR EMBL: AF138301; AAF61437.1; -
DR EMBL: AF138302; AAD44714.1; -
DR EMBL: AF138303; AAF61438.1; -
DR EMBL: AF138304; AAD44715.1; -
DR EMBL: BC005322; AAH05322.1; -
DR PIR: A26476; NBHUC8.
DR PIR: S05640; S05640.
DR PIR: B28457; B28457.
DR PIR: A45016; A45016.
DR GENE: HGNC:2705; DCN.
MIM: 125255; -
DR InterPro: IPR001611; LRR.
DR InterPro: IPR00372; LRR Nterm.
DR InterPro: IPR003592; LRR out.
DR InterPro: IPR003591; LRR typ.
DR Pfam: PF00560; LRR; 7.
DR Pfam: PF01462; LRRNT; 1.
DR SMART: SM00370; LRR; 3.
DR SMART: SM00013; LRRNT; 1.
DR SMART: SM00369; LRR_TYP; 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal; Alternative splicing; Polymorphism.
FT SIGNAL 1 16
FT PROPEP 17 30
FT CHAIN 31 359
FT DOMAIN 54 67
FT REPEAT 73 93
FT REPEAT 94 117
FT REPEAT 118 141
FT REPEAT 142 162
FT REPEAT 163 186
FT REPEAT 187 212
FT REPEAT 213 233
FT REPEAT 234 257
FT REPEAT 258 281
FT REPEAT 282 304
FT REPEAT 305 334
FT REPEAT 335 359
FT DISULFID 34 67
FT DISULFID 313 346
FT CARBOHYD 34 34
FT CARBOHYD 211 211
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT VARSPLIC 71 179
FT VARSPLIC 73 219
FT VARSPLIC 109 295
FT VARSPLIC 172 75
FT VARSPLIC 76 359
FT VARIANT 273 273
FT CONFLICT 37 37
FT CONFLICT 45 45
FT CONFLICT 45 45
SQ SEQUENCE 359 AA; 39746 MW; FF51B871A1A52DD CRC64;

FT	PROPEP	17	30
FT	CHAIN	31	360
FT	DOMAIN	55	68
FT	CYS-RICH.		
FT	REPEAT	74	94
FT	LRR-S 1.		
FT	LRR-T 1.		
FT	LRR-T 2.		
FT	LRR-S 2.		
FT	LRR-T 3.		
FT	LRR-T 4.		
FT	LRR-S 3.		
FT	LRR-T 5.		
FT	LRR-T 6.		
FT	LRR-S 4.		
FT	LRR-T 7.		
FT	LRR-T 8.		
FT	BY SIMILARITY.		
FT	BY SIMILARITY.		
FT	O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY).		
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).		
SQ	SEQUENCE	360 AA; 39837 MW; 71E84DA2D87552C0 CRC64;	
Query Match 47.3%; Score 943; DB 1; Length 360;			
Best Local Similarity 49.1%; Pred. No. 3e-58;			
Matches 186; Conservative 69; Mismatches 102; Indels 22; Gaps			
Qy	1	MKEYVLLFLALCS-AKPFPSHSIALKNMMLKDMDTDDDDDDDDDDDDDDDDDDDDNSLPFTR	59
Db	1	MKATIFELLVAQSWAGPF---QQKGLDFFML-----EDEASGIGPEEHFPVEPI	48
Qy	60	EPRSHFFFDLFPMPGPCOCYSRVHVCSDLGTSVTPTNIPFDTMLDLQNKKIKEEN	119
Db	49	EP-----MGVPCCPCQCCHLRVQCSDLGEKVPKDLPDPPTALLDLQNNKITKG	100
Qy	120	DFKGLTSLYLINNNKLTIHKFAFTTKRLRRLYLSHNQLSEIPLNLPKSIAELRIHE	179
Db	101	DFKNLNHLTLILNNKISKISPCAFAPLVKLERLYLSKNQLKEPKMPTIQELRVHE	160
Qy	180	NVKYKIOKDTFGKMNALHVLEMSANPLDNNGIEPGAEGV-TVPHIRIAEAKITSPVKGL	238
Db	161	NEITKVRKSVFNGLNQIMVVVELGTNPCLKSSGIENGAFQGMMKLSYTRIADNTTTIPQGL	220
Qy	239	PPTLELHDYNKISTVELEDKFYKRELORLGLGNKKITDIENGSLANIIPVREIHLENN	298
Db	221	PPSITELHLDGNKITKYDAASLGLNLAKLGLSFNISAVDNGSLANTPHLEHLNNN	280
Qy	299	KLKIPSGLPKELYQTIFIHLSNSIARGVNDFCPTVPKMKKLSAISLSFNPNPVKWEK	358
Db	281	KLAQPGGVADHKYIQVYVLHNNNISAIKSNDFCPGNYTKKASVGSVLSFNVPQYWEI	340
Qy	359	QPATERCVLSRMVSVOLGNF 377	
Db	341	QPSTFRCYVRAAVALGNI 359	
RESULT 17			
PGS2_RABIT			
ID	PGS2_RABIT	STANDARD;	PRT; 360 AA.
AC	Q28858; Q28608;		
DT	15-JUL-1999 (Rel. 38, Created)		
DT	15-JUN-1999 (Rel. 38, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Decorin precursor (Bone proteoglycan II) (PG-S2).		
GCN	DCN.		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_TaxID=9986;		
RX	[1]		
RP	SEQUENCE=From N.A.		
RC	TISSUE=Cornea;		

```

RX MEDLINE=95122319; PubMed=7822148;
RA Zhan Q., Burrows R., Cinton C.;
RT "Cloning and in situ hybridization of rabbit decorin in corneal
RL tissues.";
RL Invest. Ophthalmol. Vis. Sci. 36:206-215(1995).
RN [2]
RP SEQUENCE OF 38-358 FROM N.A.
RC TISSUE=Cartilage;
RA Hering T.M., Kollar J.;
RT "The primary structure of rabbit chondrocyte decorin deduced from
RL nucleotide sequence.";
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May affect the rate of fibrils formation (By
CC similarity).
CC -!- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- PTM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SLRPS) FAMILY. CLASS I SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: S76584; AAC33083.1; -
CC EMBL: U03394; AAC04315.1; -
CC InterPro: IPR001611; LRR.
CC InterPro: IPR000372; LRR_Nterm.
CC InterPro: IPR003592; LRR_Out.
CC InterPro: IPR003591; LRR_Typ.
CC Pfam: PF00560; LRR_7.
CC Pfam: PF01462; LRRNT_1.
CC SMART: SM00370; LRR; 1.
CC SMART: SM00013; LRRNT; 1.
CC SMART: SM00369; LRR_Typ; 1.
CC Glycoprotein: Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 16
FT PROPEP 17 30
FT CHAIN 31 360
FT DOMAIN 55 68
FT REPEAT 74 94
FT REPEAT 95 118
FT REPEAT 119 142
FT REPEAT 143 163
FT REPEAT 164 187
FT REPEAT 188 213
FT REPEAT 214 234
FT REPEAT 235 258
FT REPEAT 259 282
FT REPEAT 283 305
FT REPEAT 306 335
FT REPEAT 336 360
FT DISULFID 55 68
FT DISULFID 314 347
FT CARBOHYD 34 34
FT
FT CARBOHYD 212 212
FT CARBOHYD 263 263
FT CARBOHYD 304 304
FT
FT SEQUENCE 360 AA; 39896 MW; 0B50C6756FE02369 CRC64;
SQ
Query Match 47.2%; Score 941; DB 1; Length 360;
Best Local Similarity 49.6%; Pred. No. 4.le-58;

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Matches 188; Conservative 67; Mismatches 102; Indels 22; Gaps 5;
Qy 1 MKEVLLIFALCS-AKPFSPSHALKNMMLKDMEDTDDDDDDDDDDDDDDDDNSLEPTR 59
Db 1 MTATLILLLLAQSVAQGF---QQRGLDFMLED-EASGIGPDERAPELPDLDM----- 50
Qy 60 EPRSHFFPDLFPMCPFCQCSYRVVHCSIDLTSVPTNIPFDTRMIDLQNNKIKEIKEN 119
Db 51 -----LGPVCPFCQCHLRVQCSDLGLDKVPKPLPPDPTLLDLQNNKIKEIKDG 100
Qy 120 DFKGLTSLYLILNNKLTIKHPKAFITTKLRRLYLISHNQLSEIPLNLPKSLAELRIHE 179
Db 101 DFKNLNLHALILYNNKISKISPGAFPLVKRLRYLSKNHLKELPEKMPKRSQELRAHE 160
Qy 180 NKVKIKQKDTFKGMNALHVMESANPLDNNNGIEPGAGEV-TVPHIRIAEAKLTSPVKGL 238
Db 161 NEIKVRKSVFSGMNMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADNITITPQGL 220
Qy 239 PPTLELHLDYNNKISTVELEDFKRYKELQRLGNNKITDIENGLANIPIRVRIHLENN 298
Db 221 PPSLTLELDGKNKITKIDASSLKGILNNLAKLGLSFNDISAVDNGSLANAPHLREHLNN 280
Qy 299 KLKIPSGLPKLYLOIIFLHNSNIARVGVNDFCTVPKMKKSLYSALSIFNNPKYKWM 358
Db 281 KLIRVPGGLADHKTIQVYLLNNLSVVGANDFCPPGYNTKKASYSGVLSFNPVQIWEI 340
Qy 359 QPATFRCLVSRMSVQLGNF 377
Db 341 QPSTFRCLVSRMSVQLGNF 359

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RESULT 18

PGS2_HORSE STANDARD; PRT; 360 AA.

AC 046542;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Decorin precursor (Bone proteoglycan II) (PG-S2) (Dermatan sulfate proteoglycan II) (DS-PGII).

GN DCN

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OX NCBI_TaxID=9796;

RN [1]

RP SEQUENCE FROM N.A.

RA Richardson D.W., Dodge G.R.;

RT "Effects of interleukin-1 beta and tumor necrosis factor-alpha on the expression of matrix related genes in cultured equine articular chondrocytes.";

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: May affect the rate of fibrils formation (By similarity).

CC -!- SUBUNIT: Binds to type I and type II collagen, to fibronectin and TGF-beta. Forms a ternary complex with MFAP2 and ELN (By similarity).

CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).

CC -!- PTM: The attached glycosaminoglycan chain can be either chondroitin sulfate or dermatan sulfate depending upon the tissue of origin (By similarity).

CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRPS) FAMILY. CLASS I SUBFAMILY.

CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).

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FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 360 AA; 39980 MW; 99BEE1A9C812906 CRC64;

Query Match 46.9%; Score 934; DB 1; Length 360;
Best Local Similarity 49.1%; Pred. No. 1.3e-57;
Matches 186; Conservative 67; Mismatches 104; Indels 22; Gaps 4;

QY 1 MKEYVLLFLALCS-AKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDSDNSLFPTR 59
   || : || || || || : || || : || || : || || : || || : || || : ||
Db 1 MKATIIFLLAQSWAGPF---QQRGLDFMLDEASGIGPEDRAPDMPDLE----- 49

QY 60 EPRSHFPFDFLFWPCPGCOCYSRVVHCSDGLTSTVPTNIPDTRMLDLQNNKIKEKEN 119
   | : || || || || || || || || || || || || || || || || || || ||
Db 50 -----LLGVCVPCRCOCHLRVVOCSDLGLDKVFKDLPPTTLLDLQNNKITEIKDG 100

QY 120 DFGLTSLYGLILNNKLTIKHPKAFITTKKRLRLYLSHNLSEIPLNPKSLAEIRIHE 179
   || | : || || || || || || || || || || || || || || || || || ||
Db 101 DFNKLNHLHTLLVNNKISKISPCATPPLKLERLYLSKNHLKELPEKPKTLQELRAHE 160

QY 180 NKVKIKOKDFKGMNALHVLMSANPLDNNNGIEGAFEGV-TVFHTRIAEAKLTSVPKGL 238
   || : || : || : || : || : || : || : || : || : || : || : || : ||
Db 161 NEITKVRKAVFNGLNQMVVELGTNPLKSSGIENGAFQGMKLSYIRIADNTITTIPOGL 220

QY 239 PPTLLEHLHDYKISTVLEDFKRYKELORLGLGNKKTIDIEGSLANIPRVREIHLNN 298
   || : || || || || || || || || || || || || || || || || || || ||
Db 221 PPSUTLHLEGNKITKVDASSLKLGNLANLAKGLSFSNISAVDNGTLANTPHURELHNN 280

QY 299 KLKIPSGLPKLYLQIIFLHNSIARVGVNDPCVPKMKSLYSALSISLNNPVKYWEM 358
   || : || || || || || || || || || || || || || || || || || || ||
Db 281 KLIRVPGGLAEHYIQVYVYLNHNISAVGSDNDFCPGYNTKASYSVSLFNPVQYWEI 340

QY 359 OPATFRVCVLSRMSVOLGNF 377
   || : || || || || || || || || || || || || || || || || || || ||
Db 341 QPSTFRVCVYVRSALOLGN 359

RESULT 20
PGS2_MOUSE STANDARD; PRT; 354 AA.
AC P28654;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE decorin precursor (Bone proteoglycan II) (PG-S2) (PG40).
GN DCN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIH Swiss; TISSUE=Fibroblast;
RA Naïtoh Y., Suzuki S.;
RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95050610; PubMed=7961765;
RA Schoelzen T., Solursh M., Suzuki S., Reiter R., Morgan J.L.,
RA Buchberg A.M., Sacchar L.D., Iozzo R.V.;
RT "The murine decorin. Complete cDNA cloning, genomic organization,
RT chromosomal assignment, and expression during organogenesis and
RT tissue differentiation.";
RL J. Biol. Chem. 269:28270-28281(1994).
CC -/- FUNCTION: May affect the rate of fibrils formation.
CC -/- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -/- SUBCELLULAR LOCATION: Extracellular matrix.
CC -/- PTM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -/- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS

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CC (SIRPS) FAMILY, CLASS I SUBFAMILY.
CC -/- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC -----
CC EMBL: X53929; CAA37876.1; -.
DR PIR: S20812; S20812.
DR HSP: P23945; 1XUN.
DR MGD: MGI:94872; Dcn.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR00372; LRR_Nterm.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR003591; LRR_typ.
DR Pfam: PF00560; LRR; 9.
DR SMART: PF01462; LRRNT; 1.
DR SMART: SM0013; LRR; 2.
DR SMART: SM00013; LRRNT; 1.
DR SMART: SM00369; LRR_Typ; 2.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
FT SIGNAL 1 16 POTENTIAL.
FT PROPEP 17 30
FT CHAIN 31 354 DECORIN.
FT DOMAIN 49 62 CYS-RICH.
FT REPEAT 68 88 LRR-S 1.
FT REPEAT 89 112 LRR-T 1.
FT REPEAT 113 136 LRR-T 2.
FT REPEAT 137 157 LRR-S 2.
FT REPEAT 158 181 LRR-T 3.
FT REPEAT 182 207 LRR-T 4.
FT REPEAT 208 228 LRR-S 3.
FT REPEAT 229 252 LRR-T 5.
FT REPEAT 253 276 LRR-T 6.
FT REPEAT 277 299 LRR-S 4.
FT REPEAT 300 329 LRR-T 7.
FT REPEAT 330 354 LRR-T 8.
FT DISULFID 49 62 BY SIMILARITY.
FT DISULFID 308 341 BY SIMILARITY.
FT CARBOHYD 34 34 O-LINKED (GLYCOSAMINOGLYCAN) (BY
FT SIMILARITY).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 354 AA; 39809 MW; F05B5CC08DCABF6F CRC64;

Query Match 45.6%; Score 907.5; DB 1; Length 354;
Best Local Similarity 52.0%; Pred. No. 8.3e-56;
Matches 170; Conservative 65; Mismatches 87; Indels 5; Gaps 2;

QY 56 PPTREPRSHFPFD----LFWPCPGCOCYSRVVHCSDGLTSTVPTNIPDTRMLDLQNN 111
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 27 FMLEDEASGIIPYDNDPLISMCPYRCOCHLRVVOCSDLGLDKVFKDLPPTTLLDLQNN 86

QY 112 KIKETKENDFKGLTSLYGLILNNKLTIKHPKAFITTKKRLRLYLSHNLSEIPLNPKS 171
   || || || || || || || || || || || || || || || || || || || ||
Db 87 KITEKEGAFNKLDTLLVNNKISKISPEAFKPLVKLERLYLSKNHLKELPEKMPRT 146

QY 172 LAELRIHNKVKKIOKDFKGMNALHVLMSANPLDNNNGIEGAFEGV-TVFHTRIAEAK 230
   || || || || || || || || || || || || || || || || || || || ||
Db 147 LOELRVHNEITKLRKSDFNGLNNVLIETLGNPLKNSGIENGAFQGLKLSYIRISDTN 206

QY 231 LTSVPKGLPPTLLEHLHDYKISTVLEDFKRYKELORLGLGNKKTIDIEGSLANIPRV 290
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 207 ITAIPQGLPPTSUTEVHLDGNKITKVDAPSLKGLNLSKLSFSNITVWENGSLANPHL 266

QY 291 REIHLNENKKNKIPSGLPKLYLQIIFLHNSIARVGVNDPCVPKMKSLYSALSISLNF 350

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PGS1_PIG
ID PGS1_PIG STANDARD; PRT; 272 AA.
AC Q9GK06: Q9TTB5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1)
DE (Fragments).
GN BGN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE OF 1-137 FROM N.A.
RC TISSUE=Aorta;
RA Zhao B.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 138-272 FROM N.A.
RC TISSUE=Skin;
RA Wang J.F., Boykiw R.H., Reno C.R., Olson M.E., Hart D.A.;
RT "Cloning and sequencing of porcine matrix molecules.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May be involved in collagen fiber assembly (By
CC similarity).
CC -!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- TISSUE SPECIFICITY: Found in several connective tissues, specially
CC in articular cartilages.
CC -!- PTM: The two attached glycosaminoglycan chains can be either
CC chondroitin sulfate or dermatan sulfate (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
CC (SLRPS) FAMILY. CLASS I SUBFAMILY.
CC -!- SIMILARITY: CONTAINS AT LEAST 9 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC -----
DR EMBL; AF054449; AAG39274.1; -.
DR EMBL; AF159382; AAF19153.1; -.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF01462; LRRNT; 1.
DR Pfam; PF00560; LRR; 4.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_Typ; 1.
DR Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; signal.
FT SIGNAL 1 19
FT PROPEP 20 37
FT CHAIN 38 272
FT DOMAIN 64 77
FT REPEAT 83 103
FT REPEAT 104 127
FT REPEAT 128 >137
FT NON_CONS 137 138
FT REPEAT <138 152
FT REPEAT 153 173
FT REPEAT 174 197
FT REPEAT 198 221
FT REPEAT 222 244
FT REPEAT 245 >272
FT CARBOHYD 42 42
FT CARBOHYD 48 48

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FT DISULFID 64 77
FT NON_TER 272 272
SQ SEQUENCE 272 AA; 30457 MW; 6EBBAD0EF86378BB CRC64;

Query Match 32.28; Score 641; DB 1; Length 272;
Best Local Similarity 39.18; Pred. No. 1.5e-37; Indels 90; Gaps 5;
Matches 138; Conservative 52; Mismatches 73;

QY 4 YVLLFLALCSAKPFFPSHIALKNMMLKMDTDDDD-----DDDDDDDDDDNSLFT 58
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 WLLASLLALSQALPEQ-----KAFWDTLDDGLPLNDEGASGADSTSGI--- 50
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 59 REPRSHFPFDLFPMPGPGCOYCVHSCDLGTSVPTNPFTPTMLDLDONNKIKEKE 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 51 --PDLALPPTFSAMCPFGCHLRVQCSDGLKAVKPEISPDITLLDQNNDISELRK 108
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 119 NDFKGLTSLYGLILNNKLTHTKPKAFITTKRLRLYLHSHQLSEIPLNLPKSLAELRIH 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 109 DDFGLQLHYALVLVNNKISR-----STR----- 133
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 179 ENKVKKIQKDTFKGMNALHVLMSANPLDNNNGIEFGVTVFPHIRIAEAKLTSVPKGL 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 134 -----PSAPDGLKLVLRISSEAKLTGPKDL 159
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 239 PPTLELHLDYNKISTVEDEPKRYKELQRLGLGNKKTIDENGLANIPRVREIHLENN 298
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 160 PETLNELHLDHKNIOAIELELLRYSKLYRLGLGHQNRMIENGSLSFPLTRLEHLDNN 219
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 299 KKKTKPSGLPELKYLIQITFLHSNRIARVNDPCFVTPVKMKSKLYSAISLNN 351
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 220 KLSRVFAGLPDLKLLQVYLLHTNNITKGVNDPCFVGVRAYNGISLNN 272
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 23
PGS1_RABIT
ID PGS1_RABIT STANDARD; PRT; 135 AA.
AC O46377;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Biglycan (Bone/cartilage proteoglycan I) (PG-S1) (Fragment).
GN BGN.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white;
RX MEDLINE=99037997; PubMed=9822203;
RA Boykiw R.H., Sciore P., Reno C.R., Marchuk L., Frank C., Hart D.A.;
RT "Altered levels of extracellular matrix molecules mRNA in healing
RT rabbit ligaments.";
RL Matrix Biol. 171:371-378(1998).
CC -!- FUNCTION: May be involved in collagen fiber assembly (By
CC similarity).
CC -!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- TISSUE SPECIFICITY: Found in several connective tissues, specially
CC in articular cartilages.
CC -!- PTM: The two attached glycosaminoglycan chains can be either
CC chondroitin sulfate or dermatan sulfate (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
CC (SLRPS) FAMILY. CLASS I SUBFAMILY.
CC -!- SIMILARITY: CONTAINS AT LEAST 6 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC CC EMBL: AF020290; AAC39515.1; -
CC CC InterPro: IPR001611; LRR.
CC CC InterPro: IPR003591; LRR_Typ.
CC CC Pfam: PF00560; LRR; 5.
CC CC SMART: SM00369; LRR_Typ; 1.
CC KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
CC Leucine-rich repeat.
FT NON_TER 1
FT REPEAT <1 15 LRR-T 4.
FT REPEAT 16 35 LRR-S 3.
FT REPEAT 37 60 LRR-T 5.
FT REPEAT 61 84 LRR-T 6.
FT REPEAT 85 107 LRR-S 4.
FT REPEAT 108 >135 LRR-T 7.
FT NON_TER 135
SQ SEQUENCE 135 AA; 15323 MW; EFDC6E74D42F5098 CRC64;

Query Match 22.2%; Score 442; DB 1; Length 135;
Best Local Similarity 59.3%; Pred. No. 3.5e-24;
Matches 80; Conservative 30; Mismatches 25; Indels 0; Gaps 0;

Qy 217 EGVTVFHRIAIAKLTSPKGLPPTLLEHLDYNNKISTVELEDFKRYKELQRLGLGNKI 276
Db 1 DGLKINYLRISSEAKLTGIPDLPETLNLHLDHNNKIQAIIELEDLRYSKLYRGLGHNQI 60

Qy 277 TDINGSLANTPRVREIHLNENKLIKIPSGLPKLYQLIIFLHNSNISTARVGNDFCPTVP 336
Db 61 RMIENGSLFELPTRELHLDNNKLSRVAGLPDLKLQVVLHSLNNTIKVGNDFCVPVF 120

Qy 337 KWKKSLSAISLNN 351
Db 121 GVKRAYNGISLNN 135

RESULT 24
LUM_CHICK STANDARD; PRT; 343 AA.
AC P51890;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lumican precursor (Keratan sulfate proteoglycan lumican) (KSPG
DE lumican).
GN LUM OR LDC.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92112674; PubMed=1370446;
RA Bloembergen T.C., Vergnes J.-P., Hempel J., Hassell J.R.;
RT "cDNA to chick lumican (corneal keratan sulfate proteoglycan) reveals
RT homology to the small interstitial proteoglycan gene family and
RT expression in muscle and intestine.";
RL J. Biol. Chem. 267:347-352(1992).
RN [2]
RP SEQUENCE OF 79-85; 155-167 AND 246-256, AND CARBOHYDRATE-LINKAGE SITES
RP ASN-91; ASN-165 AND ASN-257.
RC TISSUE=Cornea;
RX MEDLINE=98211990; PubMed=9545293;
RA Dunley J.R., Neame P.J., Vergnes J.-P., Hassell J.R.;
RT "Identification of the N-linked oligosaccharide sites in chick corneal
RT lumican and keratan that receive keratan sulfate.";
RL J. Biol. Chem. 273:9615-9621(1998).
CC -!- SUBUNIT: Binds to laminin (By similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- TISSUE SPECIFICITY: Cornea and other tissues.
CC -!- PTM: Binds keratan sulfate chains.

-!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
(SLRPS) FAMILY, CLASS II SUBFAMILY.
-!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).

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RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBUNIT: Binds to laminin (By similarity).
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
 CC -!- TISSUE SPECIFICITY: Cornea and other tissues.
 CC -!- DEVELOPMENTAL STAGE: Present in the extracellular matrix of human
 CC articular cartilage at all ages, although its abundance is far
 CC greater in the adult. In the adult cartilage laminan exists
 CC predominantly in a glycoprotein form lacking keratan sulfate,
 CC whereas the juvenile form of the molecule is a proteoglycan.
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
 CC (SLRPS) FAMILY. CLASS II SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
 CC -----
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 CC -----
 DR EMBL; U18728; AAA85268.1; -;
 DR EMBL; U21128; AAA91639.1; -;
 DR EMBL; BC007038; AAH07038.1; -;
 DR Genew; HGNC:6724; LUM.
 DR MIM; 600616; -;
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000372; LRR_Nterm.
 DR InterPro; IPR003592; LRR_Out.
 DR InterPro; IPR003591; LRR_typ.
 DR Pfam; PF00560; LRR; 9.
 DR Pfam; PF01462; LRRNT; 1.
 DR SMART; SM00370; LRR; 4.
 DR SMART; SM00043; LRRNT; 1.
 DR SMART; SM00369; LRR_typ; 8.
 KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 KW Leucine-rich repeat; Signal.
 FT SIGNAL 1 18 BY SIMILARITY.
 FT CHAIN 19 338 LUMICAN.
 FT DOMAIN 37 53 CYS-RICH.
 FT REPEAT 59 78 LRR-S 1.
 FT REPEAT 79 102 LRR-T 1.
 FT REPEAT 103 128 LRR-T 2.
 FT REPEAT 129 149 LRR-S 2.
 FT REPEAT 150 171 LRR-T 3.
 FT REPEAT 172 196 LRR-T 4.
 FT REPEAT 197 217 LRR-S 3.
 FT REPEAT 218 241 LRR-T 5.
 FT REPEAT 242 266 LRR-T 6.
 FT REPEAT 267 286 LRR-S 4.
 FT REPEAT 287 316 LRR-T 7.
 FT REPEAT 317 338 LRR-T 8.
 FT DISULFID 295 328 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
 FT (POTENTIAL).
 FT 127 127 N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
 FT (POTENTIAL).
 FT 160 160 N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
 FT (POTENTIAL).
 FT 252 252 N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
 FT (POTENTIAL).
 FT 27 27 L -> P (IN REF. 1).
 FT CONFLICT 101 101 L -> V (IN REF. 1).
 FT CONFLICT 338 AA; 38429 MW; 905D2EBD370CC59D CRC64;
 SQ SEQUENCE
 Query Match 19.6%; Score 390; DB 1; Length 338;
 Best Local Similarity 31.8%; Pred. No. 4.2e-20;
 Matches 100; Conservative 70; Mismatches 122; Indels 22; Gaps 10;
 QY 66 PPFDFL-----PWCFFGQC-----YSRVHCSDLGLTSVPTNIPFTRMLDIGNWKIKEKE 118
 DB 25 PFLSIYGSSPNCAPCECNCPESYPSAMYCDLKLKSPM-VPPGIKLYLRRNQIDHIDE 83

QY 119 NDFKGLTSLYLILNNKL--TKIHPKAFUTTKKRLRLYLHSHNOLSEIPLNLPKSLAE 176
 DB 84 KAFENVTDQLWLIDHNLLENSKIKGRVFSKQLKQLKHLHNNHNLTSVGPPLPKSLEDLQ 143
 QY 177 IHENKVKIKQDTFKGMNALHVLMSANPLDNNNGIEFGAFEGV-TVFHIRIAEAKLTSPV 235
 DB 144 LTHNKITKL--GSFEGVLNLTFFIHLQHNLKEDAVS-AAFKGLKSLLEYLDLSFNQIARLP 200
 QY 236 KGLPPTLLEHLHDYKISTVELEDFPKRYKELQRLGIGLNKKITDIE-NGSLANIPRVREIH 294
 DB 201 SGLPVSLLTLYLDNNKISNIPDEYKFRNALQVLRSLHNLADSGIPGNSFNVSSELD 260
 QY 295 LENNKLKIPSGLPK--VLOIIFLHNSIARVGVNDVCTVTPVKMKKSLYSALSIFNNP 352
 DB 261 LSYNKLKNIPTVNEINENLYLEV-----NOLEKFDIKSPCKILGLOPLYSYKIKHLRDG 315
 QY 353 VKYEMQOPATFRVCV 366
 DB 316 ISETSLPPDMYECL 329
 RESULT 27
 LUM_BOVIN
 ID LUM_BOVIN STANDARD; PRT; 342 AA.
 AC Q05443;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Luminan precursor (Keratan sulfate proteoglycan) (KSPG) (Corneal
 DE keratan sulfate proteoglycan 37B core protein).
 GN LUM OR LDC.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 272-295.
 RC TISSUE=Cornea;
 RX MEDLINE=93280153; PubMed=8099356;
 RA Funderburgh J.L., Funderburgh M.L., Brown S.J., Vergnes J.-P.,
 RA Hassell J.R., Mann M.M., Conrad G.W.;
 RT "Sequence and structural implications of a bovine corneal keratan
 RT sulfate proteoglycan core protein. Protein 37B represents bovine
 RT luminan and proteins 37A and 25 are unique.";
 RL J. Biol. Chem. 268:11874-11880(1993).
 RN [2]
 RP SEQUENCE OF 19-42.
 RX MEDLINE=90243714; PubMed=2139877;
 RA Funderburgh J.L., Conrad G.W.;
 RT "Isoforms of corneal keratan sulfate proteoglycan.";
 RL J. Biol. Chem. 265:8297-8303(1990).
 CC -!- SUBUNIT: Binds to laminin.
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
 CC -!- TISSUE SPECIFICITY: Cornea and other tissues.
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
 CC (SLRPS) FAMILY. CLASS II SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L11063; AAA30608.1; -;
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000372; LRR_Nterm.
 DR InterPro; IPR003592; LRR_Out.
 DR InterPro; IPR003591; LRR_typ.

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DR Pfam; PF00560; LRR; 9.
DR Pfam; PF01462; LRRNT; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00370; LRR; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_Typ; 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT CHAIN 1 18
FT SIGNAL 19 342
FT DOMAIN 41 57
FT REPEAT 63 82
FT REPEAT 83 106
FT REPEAT 107 132
FT REPEAT 133 153
FT REPEAT 154 175
FT REPEAT 176 200
FT REPEAT 201 221
FT REPEAT 222 245
FT REPEAT 246 270
FT REPEAT 271 290
FT REPEAT 291 320
FT REPEAT 321 342
FT DISULFID 299 332
FT CARBOHYD 92 92
FT CARBOHYD 131 131
FT CARBOHYD 164 164
FT CARBOHYD 256 256
FT CARBOHYD 342 AA; 38756 MW; 592DEE9A489AEB79 CRC64;
SQ
Query Match 19.3%; Score 384; DB 1; Length 342;
Best Local Similarity 32.2%; Pred. No. 1.1e-19;
Matches 101; Conservative 68; Mismatches 123; Indels 22; Gaps 10;
QY 66 FPFDFP---PMCPFGQC---YSRVHCHSDGLGTSVPTNPDPTRMLDNNKKIKEIKE 118
Db 29 FPQALYGRSSPNCAPCEPCSPSAPMCDLKLKSVPM-VPPGKLYLRLNNQIDHDD 87
QY 119 NDFKGLTSLGLILNNKL--TKTHPKAFLTKKRLRLYLHSHNQLSEIPLNLPKSLAE 176
Db 88 KAPENVTDLOWLILDHNLLENKSKIKGVFSKQLKQLKHLHYNLNLTESVGPLPKSLVDLQ 147
QY 177 IHENKVKIKQDFTKGMNALHVLMSANPLDNNNGIEPFAFEGV-TVPHIRIAEAKLTSVP 235
Db 148 LTNNKISKL--GSPDGLVNLTFIHLQNLKEDAVS-AALKGLKSLLEYLDLSFNQMKLP 204
QY 236 KGLPPTLLELDYNNKISTVELEDFRYKELQRLGLGNKKITDI-ENGSLANIPRVREIH 294
Db 205 SGLVSLTLYLDNNKISNIPDEYFRFSALQYLRSLHNLADSGVPGNSFNVSLSLELD 264
QY 295 LENKKKIPSGLPKLK--YLOIFLHNSIARVGNDFCPTVPKMKKSLYSALISFNPP 352
Db 265 LSNKLSKISFTVNNLENYILEV-----NELEKEDVKSFKILGPLYSKIKHLRLDGNH 319
QY 353 VKYEMQPATFRCV 366
Db 320 ITQTSLPDMVECL 333
RESULT 28
LUM_MOUSE
ID LUM_MOUSE STANDARD; PRT; 338 AA.
AC P51885; Q9CXK0; Q99JZ3;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Luminican precursor (Keratan sulfate proteoglycan lumican) (KSPG
DE lumican).
GN LUM OR LDC OR LCN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cornea;
RX MEDLINE=96006258; PubMed=7558724;
RA Funderburgh J.L., Funderburgh M.L., Hevelone N.D., Stech M.E.,
RA Justice M.J., Liu C.-Y., Kao W.W.-Y., Conrad G.W.;
"Sequence, molecular properties, and chromosomal mapping of mouse
lumican.";
RL Invest. Ophthalmol. Vis. Sci. 36:2296-2303(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boiffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBUNIT: Binds to laminin (By similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- TISSUE SPECIFICITY: Cornea and other tissues.
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC -!- (SLRPS) FAMILY. CLASS II SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; S79461; AAB35361.1; -.
CC EMBL; AF013262; AAB87767.1; -.
CC EMBL; AK014312; BAB29284.1; -.
CC EMBL; BC005550; AAH05550.1; -.
CC MGD; MGI:109347; Lum.
CC InterPro; IPR001611; LRR.
CC InterPro; IPR000372; LRR_Nterm.
CC InterPro; IPR003592; LRR_out.
CC InterPro; IPR003591; LRR_Typ.
CC Pfam; PF00560; LRR; 9.
CC Pfam; PF01462; LRRNT; 1.

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DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00370; LRR; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_TYP; 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
FT SIGNAL 1 18
FT CHAIN 19 338
FT DOMAIN 37 53
FT REPEAT 59 78
FT REPEAT 79 102
FT REPEAT 103 128
FT REPEAT 129 149
FT REPEAT 150 171
FT REPEAT 172 196
FT REPEAT 197 217
FT REPEAT 218 241
FT REPEAT 242 266
FT REPEAT 267 286
FT REPEAT 287 316
FT REPEAT 317 338
FT DISULFID 295 328
FT CARBOHYD 88 88
FT CARBOHYD 127 127
FT CARBOHYD 160 160
FT CARBOHYD 252 252
FT CONFLICT 57 57
FT CONFLICT 109 109
FT CONFLICT 293 293
FT CONFLICT 338 AA; 38265 MW; FE1E050C89779140 CRC64;
SQ SEQUENCE 338 AA; 38265 MW; FE1E050C89779140 CRC64;

Query Match 19.2%; Score 383; DB 1; Length 338;
Best Local Similarity 32.9%; Pred. No. 1.3e-19;
Matches 100; Conservative 66; Mismatches 120; Indels 18; Gaps 9;

QY 72 PNCPCGOC---YSRVHCSDGLTSVPTNIPFDTMLDLQNNKIKEIKENDFKGLTSLY 128
Db 35 PNCPCGOC---YSRVHCSDGLTSVPTNIPFDTMLDLQNNKIKEIKENDFKGLTSLY 128
QY 129 GLILNNKL--TKIHPKAFLLTKLRLYLSHNSLSEPLNPKSLAEIRHENKVKIQ 186
Db 94 WLILDHNLLENSKIKGVFSKQLKQLKHLHYNLNTESVGPLPKSLQDLQTLNNKISKL- 152
QY 187 KDTFGKMAHLVLEMSANPLDNNNGIEPGAFGV-TVPHIRIAEAKLTSVPKGLPPTLLEL 245
Db 153 -GSFDGLVNLTFIYLOHNLQKEDAVS-ASLGLKSLEYLDLSFNQMSKLPAGLPTSLTL 210
QY 246 HLDYNNKISTVEDEPKRYKELQRLGLNNKTTDI-ENGSLANIPRVREIHLNNKLLKIP 304
Db 211 YLDNNKISNIPDEYFKRTGLQYLRSLHNEADSGVGNFNSISLLELDLSYNKLSKIP 270
QY 305 SGLPELK--YIQIIFLHNSIARVGNDFCTVPKMKKLSYSAISLNNPNVYKWMOPAT 362
Db 271 TVNENLNNYILEV-----NELEKFDVKSFKILGLPLSKIKHLRLDGNPLTQSSLPDM 325
QY 363 FCV 366
Db 326 YEC 329

RESULT 29
LUM_RAT
ID LUM_RAT STANDARD; PRT; 338 AA.
AC P51886;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lumican precursor (Keratan sulfate proteoglycan lumican) (KSPG lumican).

GN LUM OR LDC OR LCN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Eye;
RA Krull N.B.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SUBUNIT: Binds to laminin (By similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPs) FAMILY, CLASS II SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC -----
CC EMBL; X84039; CAA58858.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00560; LRR; 9.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00370; LRR; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_TYP; 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 18
FT CHAIN 19 338
FT DOMAIN 37 53
FT REPEAT 59 78
FT REPEAT 79 102
FT REPEAT 103 128
FT REPEAT 129 149
FT REPEAT 150 171
FT REPEAT 172 196
FT REPEAT 197 217
FT REPEAT 218 241
FT REPEAT 242 266
FT REPEAT 267 286
FT REPEAT 287 316
FT REPEAT 317 338
FT DISULFID 295 328
FT CARBOHYD 88 88
FT CARBOHYD 127 127
FT CARBOHYD 160 160
FT CARBOHYD 252 252
FT CONFLICT 57 57
FT CONFLICT 109 109
FT CONFLICT 293 293
FT CONFLICT 338 AA; 38265 MW; FE1E050C89779140 CRC64;
SQ SEQUENCE 338 AA; 38265 MW; FE1E050C89779140 CRC64;

Query Match 19.0%; Score 378; DB 1; Length 338;
Best Local Similarity 32.2%; Pred. No. 2.9e-19;
Matches 99; Conservative 67; Mismatches 123; Indels 18; Gaps 9;

QY 69 DLFPMPGFCQC---YSRVVHCSDGLTSVPTNIPFDTMLDLQNNKIKEIKENDFKGLT 125
Db 32 ELSPNCAPECNPHSYPTAMCYDDLLKSVPM-VPGIKYLYLRNNQIDHIDEKAFENVT 90
QY 126 SLYGLILNNKL--TKIHPKAFLLTKLRLYLSHNSLSEPLNPKSLAEIRHENKVK 183
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Db 91 DLQWILDHNLLENSKTKGVSKLKQKLUHINYNNLTESVGPLKSLQDLQLANNKIS 150
 QY 184 KTOKDTFGKGNALHVLMSANPLDNNGIEPCAFEGV-TVPHIRIAEAKLTSPKGLPPTL 242
 Db 151 KL--GSPDLVNLFIYLOHNLQKEAVS-ASLGLSKLEYLDSFNQMSKLPAGLPTSL 207
 QY 243 LELHLDYNKISTVELEDFKRYKELQRLGLGNKKTIDT-ENGLSANIPRVREIHLENNK 301
 Db 208 LTLYLDNNKITNPDEYFNRTGLQYLRSHNELADGVPNGSNFISSLELDELSSYNK 267
 QY 302 KIPSLPELK--YLOITFLHNSSTARVGVNDFCTVPKMKKSLYSALISLNNPVKYM 359
 Db 268 SPTVNNLENYLEYV-----NKLEKFDVKSFCILGLPSYSKIKHLRLDGNPLTQSSLP 322
 QY 360 PATRCV 366
 Db 323 FDMYECL 329
 RESULT 30
 OMD_HUMAN
 ID OMD_HUMAN STANDARD; PRT; 421 AA.
 AC Q99983;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Osteomodulin precursor (Osteoadherin) (OSAD) (Keratan sulfate
 proteoglycan osteomodulin) (KSPG osteomodulin).
 GN OMD.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Osteoblast;
 RA Ohno I., Hashimoto J., Takaoka K., Ochi T., Okubo K., Matsubara K.;
 RT "The cloning of a cDNA for novel genes expressed in human
 osteoblasts";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ohno I., Matsubara K., Okubo K.;
 RT "Human osteomodulin gene: intron-exon junctions and chromosomal
 localization.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May be implicated in biomineralization processes. Has a
 function in binding of osteoblasts via the alpha(V)beta(3)-
 integrin (By similarity).
 CC -!- SUBUNIT: Binds the alpha(V)beta(3)-integrin (By similarity).
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix (Potential).
 CC -!- TISSUE SPECIFICITY: Bone-specific.
 CC -!- PTM: Binds keratan sulfate chains (By similarity).
 CC -!- PTM: Sulfated on tyrosine residue(s) (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
 (SIRS) FAMILY. CLASS II SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AB000114; BAA19055.1;
 CC EMBL: AB009589; BAA23982.1;
 CC GenBank: HGNC:8134; OMD.
 CC InterPro: IPR001611; LRR.
 CC InterPro: IPR000372; LRR_Nterm.
 CC InterPro: IPR003592; LRR_Out.
 CC InterPro: IPR003591; LRR_typ.

DR pfam; PF00560; LRR; 7.
 DR SMART; PF01462; LRRNT; 1.
 DR SMART; SM00370; LRR; 1.
 DR SMART; SM00013; LRRNT; 1.
 DR SMART; SM00369; LRR_TYP; 1.
 KW Cell adhesion; Glycoprotein; Extracellular matrix; Proteoglycan;
 KW Repeat; Leucine-rich repeat; Signal; Sulfation.
 FT SIGNAL 1 20
 FT CHAIN 21 421
 FT DOMAIN 62 78
 FT REPEAT 84 103
 FT REPEAT 104 127
 FT REPEAT 128 153
 FT REPEAT 154 174
 FT REPEAT 175 198
 FT REPEAT 199 224
 FT REPEAT 225 245
 FT REPEAT 246 269
 FT REPEAT 270 292
 FT REPEAT 293 312
 FT REPEAT 313 342
 FT REPEAT 343 367
 FT DOMAIN 385 409
 FT DISULFID 321 353
 FT MOD_RES 25 25
 FT MOD_RES 31 31
 FT MOD_RES 39 39
 FT CARBOHYD 113 113
 FT CARBOHYD 121 121
 FT CARBOHYD 187 187
 FT CARBOHYD 242 242
 FT CARBOHYD 316 316
 SQ SEQUENCE 421 AA; 49492 MW; CED47B2BC33BB872 CRC64;
 Query Match 18.4%; Score 366; DB 1; Length 421;
 Best Local Similarity 29.3%; Pred. No. 2.5e-18;
 Matches 95; Conservative 73; Mismatches 138; Indels 18; Gaps 8;
 QY 41 DDDDDDDDDDDNSLFPTRPRSRHFPFDPFPM-CPFQCQC---YSRVHVCSDGLTSVP 96
 Db 28 DEDYDEPDDDYQTGFPPQNVYGVPPHGYTLGCVSECFCTNFPSSMYCDNRKLTIP 87
 QY 97 TNIPFTRMLDLONNKIKEIKENDEKGLTSLYGLILNNKLL--TKHKPAFLTTTKKRL 154
 Db 88 -NTPMHIQOYLQFNEIEAVTANFTNATHLKEINLHNKIKSQIDYGVFAKLPLQL 146
 QY 155 YLSHNSLPIPLNPKSLAELEHKNVKKIQKDTFGKGNALHVLMSANPLDNNGIEPG 214
 Db 147 HLEHNNLEFPPLPKSLERLLGYNEISKLTQTNAMDGLVNLTLMDLCYNYLHDSLLKDK 206
 QY 215 APEGV-TVPHIRIAEAKLTSPKGLPPTLLEHLDYNKISTVELEDFKRYKELQRLGN 273
 Db 207 IFAKWEKLMQLNLCNRLSEMPPLPSLMYLSLENNSSISSEIPEYFKDKLPKLTLRMSH 266
 QY 274 NKITDIENGLANIPRVREIHLENNKLLK---IPSGLELKYLOIFLHNSIARVGVND 330
 Db 267 NGLQDIPY-NIFNLPIVLSVGHNKLKQAFYIPRNLEHL-----YLNNEIERMNTV 319
 QY 331 FCPTVPKMKKSLYSALISLNNPVK 354
 Db 320 MCPSIDPLHYHHLTVIRVDONK 343
 RESULT 31
 FLRL_HUMAN
 ID FLRL_HUMAN STANDARD; PRT; 646 AA.
 AC Q9NZUL;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Leucine-rich repeat transmembrane protein FLRL precursor
 DE (Fibronectin-like domain-containing leucine-rich transmembrane protein
 1).

GN FLRT1.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND GLYCOSYLATION.
 RX MEDLINE=20112755; PubMed=10644439;
 RA Lacy S.E., Bonnemant C.G., Buzney E.A., Kunkel L.M.;
 RT "Identification of FLRT1, FLRT2, and FLRT3, a novel family of
 transmembrane leucine-rich repeat proteins.";
 RL Genomics 62:417-426(1999).
 CC -!- FUNCTION: May have a function in cell adhesion and/or receptor
 CC signaling.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
 CC -!- TISSUE SPECIFICITY: Expressed in kidney and brain.
 CC -!- PM: N-glycosylated.
 CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 10 LEUCINE-RICH REPEATS (LRR).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF169675; AAF28459.1; ALT_INIT.
 CC Genew; HGNC:3760; FLRT1.
 DR MIM; 604806; -.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR000372; LRR_Nterm.
 DR InterPro; IPR003592; LRR_Out.
 DR InterPro; IPR003591; LRR_Eyp.
 DR Pfam; PF00041; fn3; 1.
 DR Pfam; PF00560; LRR; 7.
 DR Pfam; PF01462; LRRNT; 1.
 DR Pfam; PF01463; LRRCT; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00370; LRR; 1.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00013; LRRNT; 1.
 DR SMART; SM00369; LRR_Typ; 1.
 KW Transmembrane, Leucine-rich repeat; Repeat; Glycoprotein; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 646
 FT LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN
 FT FLRT1.
 FT DOMAIN 21 524
 FT TRANSMEM 525 545
 FT DOMAIN 546 646
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT REPEAT 52 77
 FT LRR 1.
 FT REPEAT 78 98
 FT LRR 2.
 FT REPEAT 99 121
 FT LRR 3.
 FT REPEAT 123 147
 FT LRR 4.
 FT REPEAT 148 169
 FT LRR 5.
 FT REPEAT 170 192
 FT LRR 6.
 FT REPEAT 194 218
 FT LRR 7.
 FT REPEAT 219 241
 FT LRR 8.
 FT REPEAT 242 264
 FT LRR 9.
 FT REPEAT 265 288
 FT LRR 10.
 FT FIBRONECTIN TYPE-III.
 FT DOMAIN 407 485
 FT CARBOHYD 221 227
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 271 271
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 646 AA; 71359 MW; FF2BF5DC3A13C92 CRC64;
 Query Match 18.28; Score 363.5; DB 1; Length 646;
 Best Local Similarity 32.74; Pred. No. 6.4e-18;
 Matches 92; Conservative % 51; Mismatches 105; Indels 33; Gaps 7;
 OY 74 CPFGQCYSRVVHCSDLGLTSVPTNIPFDRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133

Db 26 CPSCVRCDCNGFIYCNDRLGLTSIPADIPDDATTLYLQNNQI-----N 66
 QY 134 NNKLTIKHPKAFITTKRLRLRYLSHNLSEIPLNPKSLAEIRIHENKVKYKOKDFPKM 193
 Db 67 NAGI-----PQDLTKVNVQVIVLYENDLDEFINLPSRLRELHLQDNVNRVTIARDSLARI 122
 QY 194 NALHVLMSANPLDNNNGIEGAP-EGVTVFHRIAEAKLTSVPKGLPPTLLLEHLHDYDKI 252
 Db 123 PLEKLUHLDNDSVSTVSEIEDAFADSKQLKLLFLSRNHLSSIPSGLPHTLEELRLDDNRI 182
 QY 253 STVELEDFKRYKQLRQLGLGNKKITD--IENGSLANIPRVREIHLNKKIKIPSGLP 310
 Db 183 STIPLHAFKGLNSRLRLVDGLNLANQRIADDTFSLQNLTELSELVSRNSLAAPLNLP- 241
 QY 311 KYLQIIFLHNSIARVGVNDFCTVPKMKKSLYSALSIFNN 351
 Db 242 AHLQKLYQDNATISHIPYN----TLAKMRE--LERLDLSNN 276
 RESULT 32
 PRLP_BOVIN
 ID PRLP_BOVIN STANDARD; PRT; 381 AA.
 AC Q9GKN8;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Prolargin precursor (proline-arginine-rich end leucine-rich repeat
 DE protein).
 DE GN PRELP.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Articular cartilage;
 RX MEDLINE=20576219; PubMed=1007795;
 RA Bengtsson E., Aspberg A., Heinegaard D., Sommarin Y., Spillmann D.;
 RT "The amino-terminal part of PRELP binds to heparin and heparan
 RT sulfate.";
 RL J. Biol. Chem. 275:40695-40702(2000).
 RN [2]
 RP FUNCTION
 RX PubMed=11847210;
 RA Bengtsson E., Moergelin M., Sasaki T., Timpl R., Heinegaard D.,
 RA Aspberg A.;
 RT "The leucine-rich repeat protein PRELP binds perlecan and collagens
 RT and may function as a basement membrane anchor.";
 RL J. Biol. Chem. 277:15061-15068(2002).
 CC -!- FUNCTION: May anchor basement membranes to the underlying
 CC connective tissue.
 CC -!- SUBUNIT: Binds the basement membrane heparan sulfate proteoglycan
 CC perlecan and triple helical collagens type I and type II.
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix.
 CC -!- DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin and
 CC heparan sulfate. Binds collagens type I and type II through its
 CC leucine-rich repeat domain.
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
 CC (SLRPS) FAMILY. CLASS II SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
 CC -----
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 CC -----
 CC EMBL; AF163568; AAG23723.1; -.
 DR InterPro; IPR001611; LRR.

DR	InterPro; IPR003592; LRR_out.
DR	InterPro; IPR003591; LRR_typ.
DR	Pfam; PF00560; LRR; 8.
DR	Pfam; PF01462; LRRNT; 1.
DR	PRINTS; PR00019; LEURICHRPT.
DR	SMART; SM00370; LRR; 5.
DR	SMART; SM00013; LRRNT; 1.
DR	SMART; SM00369; LRR_TYP; 8.
KW	Glycoprotein; Extracellular matrix; Repeat; Leucine-rich repeat;
KW	Signal.
FT	SIGNAL. 1 21 POTENTIAL.
FT	CHAIN 22 377 PROLARGIN.
FT	DOMAIN 68 84 CYS-RICH.
FT	REPEAT 90 109 LRR-S 1.
FT	REPEAT 110 133 LRR-T 1.
FT	REPEAT 134 157 LRR-T 2.
FT	REPEAT 158 178 LRR-S 2.
FT	REPEAT 179 202 LRR-T 3.
FT	REPEAT 203 228 LRR-T 4.
FT	REPEAT 229 249 LRR-S 3.
FT	REPEAT 250 273 LRR-T 5.
FT	REPEAT 274 298 LRR-T 6.
FT	REPEAT 299 318 LRR-S 4.
FT	REPEAT 319 337 LRR-T 7.
FT	REPEAT 358 377 LRR-T 8.
FT	DOMAIN 192 197 POLY-LEU.
FT	DISULFID 327 368 BY SIMILARITY.
FT	CARBOHYD 119 119 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 284 284 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 322 322 N-LINKED (GLCNAC. .) (POTENTIAL).
SEQ	SEQUENCE 377 AA; 43179 MW; 79CBE62534753C46 CRC64;
Query Match 17.9%; Score 356.5; DB 1; Length 377;	
Best local similarity 30.7%; Pred. No. le-17;	
Matches 84; Conservative 58; Mismatches 121; Indels 11; Gaps	
QY	67 PFDLPMPGCGQC---YSRVHVCSDLGLSVPTNPFDTRMLDLQNKKIKEKDNFKG 123
DB	61 PPSVPDCPRECYPDPFPSALYCDNSLNLRKVPI -IPRIHYLYLQNNFITELPVESFN 119
QY	124 LTSLYGLIANNKLTKLHPKRAFTTKRLRSLYLSHNQLSEIPLNLPKSLAEIRHENVKR 183
DB	120 ATGLRWINDNRIRKVDQRVEKLPGLAFLYMDKNQLEEVSPALPNLEQLSQLNIS 179
QY	184 KIQKDTFGMNAHLVEMSANPLDNGIEPGAFEGV-TVPHIRIAEAKLTSPVKGPLPPTL 242
DB	180 RIPPGVFSKLENLLLDLQHNLSDGVFKADTFQGLKNLMQLNAHLNLRMRMPKPVPAP 239
QY	243 LEHLDYNKITSTVELEDFFKRYKELQRLGLGNKITD--IENGSIANTPRVRETHLENNKL 300
DB	240 HOLYDSNKIETTPSGVFKDFPNLAIFRMYNKSDRGLPKPNKF-NISNLLVLHLSHNKI 298
QY	301 KKIPSGPELKYLQIIFLHSNSIARVGNDPCPT 334
DB	299 SNVPAISNKEHL--YLNNSIEKINGTQICPS 329
RESULT 35	
KERA_MOUSE	
ID KERA_MOUSE STANDARD; PRT; 351 AA.	
AC O35367;	
DT 15-JUN-2002 (Rel. 41, Created)	
DT 15-JUN-2002 (Rel. 41, Last sequence update)	
DT 15-JUN-2002 (Rel. 41, Last annotation update)	
DE Keratocan precursor (KTN) (keratan sulfate proteoglycan keratocan).	
GN KERA OR KTCN.	
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
NCBI_TaxID=10090;	
RN [1]	
RP SEQUENCE FROM N A	

RC STRAIN=AKR/J X C57L/J; TISSUE=Eye;
 RX MEDLINE=98191735; PubMed=9530631;
 RA Dunlevy J.R., Chakravarti S., Gyalzen P., Vergnes J.-P., Hassell J.R.;
 RT "Cloning and chromosomal localization of mouse keratocan, a corneal
 keratan sulfate proteoglycan."; Mamm. Genome 9:316-319(1998).
 RL Mamm. Genome 9:316-319(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ; TISSUE=Cornea;
 RX MEDLINE=98380483; PubMed=9712886;
 RA Liu C.-Y., Shiraishi A., Kao C.W.-C., Converse R.L., Funderburgh J.L.,
 RA Corpuz L.M., Conrad G.W., Kao W.W.-Y.;
 RT "The cloning of mouse keratocan cDNA and genomic DNA and the
 characterization of its expression during eye development."; J. Biol. Chem. 273:22584-22588(1998).
 RL J. Biol. Chem. 273:22584-22588(1998).
 CC -!- FUNCTION: May be important in developing and maintaining corneal
 transparency and for the structure of the stromal matrix.
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix (Potential).
 CC -!- TISSUE SPECIFICITY: Selectively expressed in cornea of adult where
 it is detected in keratocytes but not in scleral cells. In embryo,
 first detected in pericocular mesenchymal cells migrating toward
 developing cornea on E13.5; expression gradually restricted to
 corneal stromal cells on E14.5 to E18.5. Detected in scleral cells
 of E15.5 but not in E18.5 embryos.
 CC -!- PTM: Binds keratan sulfate chains.
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
 (SLRPS) FAMILY. CLASS II SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF022256; AAC15505.1; -;
 DR EMBL; AF057301; AAC61257.1; -;
 DR MGD; MGI:1202398; Kera.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR003772; LRR_Nterm.
 DR InterPro; IPR003592; LRR_Out.
 DR Pfam; PF00560; LRR; 8.
 DR Pfam; PF01462; LRRNT; 1.
 DR SMART; SM00370; LRR; 3.
 DR SMART; SM00013; LRRNT; 1.
 KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 KW Leucine-rich repeat; Signal; Sulfation.
 FT SIGNAL 1 20
 FT CHAIN 21 351
 FT DOMAIN 42 58
 FT REPEAT 65 84
 FT REPEAT 85 108
 FT REPEAT 109 134
 FT REPEAT 135 155
 FT REPEAT 156 179
 FT REPEAT 180 205
 FT REPEAT 206 226
 FT REPEAT 227 250
 FT REPEAT 251 275
 FT REPEAT 276 295
 FT REPEAT 308 331
 FT REPEAT 332 351
 FT DISULFID 304 342
 FT MOD_RES 27 27
 FT CARBOHYD 94 94
 FT
 FT CARBOHYD 168 168
 FT CARBOHYD 223 223
 FT CARBOHYD 299 299
 FT SEQUENCE 351 AA; 40403 MW; B0632B387864B98D CRC64;

Query Match 17.3%; Score 345; DB 1; Length 351;
 Best Local Similarity 28.1%; Pred. No. 5.7e-17;
 Matches 95; Conservative 60; Mismatches 121; Indels 62; Gaps 10;
 QY 31 LKDMEDTDDDDDDDDDDDDDDNSLFTPTREPSRSHFFPDLFPMCPFGCQC---YSRVHC 87
 DB 29 IODPEDVHDD-----FY-----CPRCFCPSPTALYC 59
 QY 88 SDLGTSVPTNIPFDTRMLDQNNKIKIKENDEKGLSTLYGLILNNKLFK--IHPKAF 145
 DB 60 ENRGLEIIPP-IPSRWIWLYLNNLIESIPEKPPENATQLRWLNKKNITNYGKCAL 118
 QY 146 LTTKKLRRLYLSHNOLSEIPLNPKSLAEIRIHENKVKYKIOKDTFGKNNALHVLMSANP 205
 DB 119 SOLKKLLFLFEDNEEVPSPRSLQQLARNVKSRIPQGTFSNIENITLLDLQHNK 178
 QY 206 LDNNGIEPGAFGV-TVFHIRIAEAKLTSPKGLPPTLLELHLDYNKISTVELEDFKRYK 264
 DB 179 LDNNAFQRTFGKLNLMQNLAKNALRMPRLPANTMQFLDNNSTEGIPENYFNVP 238
 QY 265 ELQRLGLGNKNTD-----IENGSLANIPRV-----REIHLENNKLLKKI 303
 DB 239 KVAFLRLNHNKLSADAGLPSRGFDVSSILDQLSYNQLTNFPRINANLQHLHDHNKIKNV 298
 QY 304 PSGL---PELKKYLOIIFLHNSIA--RVGVNDFCPTVP 336
 DB 299 NMSVICPTTLRAEQDAFHGPOLSYRLDGNIEKPPIP 336
 RESULT 36
 FMOD_BOVIN
 ID FMOD_BOVIN STANDARD; PRT; 375 AA.
 AC P13605;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibromodulin precursor (FM) (Collagen-binding 59 kDa protein) (Keratan
 sulfate proteoglycan fibromodulin) (KSPG fibromodulin).
 GN FMOD.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 90-105 AND 274-281.
 RX MEDLINE=90060020; PubMed=2531085;
 RA Oldberg A., Antonsson P., Lindblom K., Heinigaard D.;
 RT "A collagen-binding 59-kd protein (fibromodulin) is structurally
 related to the small interstitial proteoglycans PG-S1 and PG-S2
 (decorin).";
 RT EMBO J. 8:2601-2604(1989).
 RL [2]
 RP KERATAN SULFATE ATTACHMENT SITES.
 RX MEDLINE=91056119; PubMed=2243109;
 RA Plaas A.H.K., Neame P.J., Nivens C.M., Reiss L.;
 RT "Identification of the keratan sulfate attachment sites on bovine
 fibromodulin."; J. Biol. Chem. 265:20634-20640(1990).
 RL [3]
 RP STRUCTURE OF CARBOHYDRATES.
 RX MEDLINE=97129119; PubMed=8973659;
 RA Lauder R.M., Huckerby T.N., Nieduszynski I.A.;
 RT "The structure of the keratan sulphate chains attached to
 fibromodulin isolated from articular cartilage."; Eur. J. Biochem. 242:402-409(1996).
 CC -!- FUNCTION: Affects the rate of fibrils formation. May have a
 primary role in collagen fibrillogenesis (By similarity).
 CC -!- SUBUNIT: Binds to type I and type II collagen.
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix.
 CC -!- PTM: Binds keratan sulfate chains.
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS

DR	SMART:	SM000370;	LRR:	1.
DR	SMART:	SM00013;	LRRNT:	1.
DR	SMART:	SM00369;	LRR_TYP:	1.
KW	Glycoprotein; Extracellular matrix; Proteoglycan; Repeat; Leucine-rich repeat; Signal.			
FT	SIGNAL	1	18	BY SIMILARITY.
FT	CHAIN	19	376	FIBROMODULIN.
FT	DOMAIN	76	92	CYS-RICH.
FT	REPEAT	98	117	LRR-S 1.
FT	REPEAT	118	141	LRR-T 1.
FT	REPEAT	142	167	LRR-T 2.
FT	REPEAT	168	188	LRR-S 2.
FT	REPEAT	189	212	LRR-T 3.
FT	REPEAT	213	235	LRR-T 4.
FT	REPEAT	236	256	LRR-S 3.
FT	REPEAT	257	280	LRR-T 5.
FT	REPEAT	281	305	LRR-T 6.
FT	REPEAT	306	325	LRR-S 4.
FT	REPEAT	326	355	LRR-T 7.
FT	REPEAT	356	376	LRR-T 8.
FT	DOMAIN	68	73	POLY-PRO.
FT	DISULFID	334	367	BY SIMILARITY.
FT	CARBOHYD	127	127	N-LINKED (GLCNAC. .) (KERATAN SULFATE).
FT				(BY SIMILARITY).
FT	CARBOHYD	166	166	N-LINKED (GLCNAC. .) (KERATAN SULFATE).
FT				(BY SIMILARITY).
FT	CARBOHYD	201	201	N-LINKED (GLCNAC. .) (KERATAN SULFATE).
FT				(BY SIMILARITY).
FT	CARBOHYD	291	291	N-LINKED (GLCNAC. .) (KERATAN SULFATE).
FT				(BY SIMILARITY).
FT	CARBOHYD	341	341	N-LINKED (GLCNAC. .) (POTENTIAL).
FT				(BY SIMILARITY).
SEQ	SEQUENCE	376 AA;	43219 MW;	9C3298675CE3714A CRC64;
Query Match		17.0%;	Score 338;	DB 1; Length 376;
Best Local Similarity		28.0%;	Pred. No. 1.9e-16;	
Matches 104; Conservative		65;	Mismatches 160;	Indels 42; Gaps
QY	6	LLFLALCSAK--PFSPSHIAKNNMLK-----DMEDTDDDDDDDDDDDEDNSLF--	56	
DG	6	ILLRLGLCSLQSQGYEEDSHWLQLYLRNQOSTYYDPDYVETSDPYPEVEEGPAYAY	65	
QY	57	--PTREPGRSHFFDFLMCPGCCQC---YSRVHCSDLGLTSVPTNPFDTRMLDLQN	110	
DG	66	GAPPPPEPRD-----CPOECDCPPNFTAMYCDNRNLKYLFP-VPSRKKYVYFON	114	
QY	111	NKIKETKENDFKGLTSLYGLILNNKKLT--KIHPKAFLTTKKLRRLYLSHNQISEPLNL	168	
DG	115	NQLAAIQEGVFADNATGLLWIALHGNOITSDKIGRKVFSKLRLHLRYLDHNNLTRMPGPL	174	
QY	169	PKSLAEURLTHENVKVIQKDTFKGKNALHVLEMSANPLDNNGIEPGAFGV-TVFHRIA	227	
DG	175	PRSRLRELHDHNOISRPVNNALEGLENLTALYLHHNEIQEVG---SSMRGLASLIILLDS	231	
QY	228	EAKLTSVPKGLPTLLELHDYANKISTVELEDPKRYKELORGLGNKTKTDIENGSLA--	285	
DG	232	YNHLRRVPDGLSALQCLYLEHNNVTVPDSPERGSPKLLYVRLSHNSTUT---NNGLATN	288	
QY	286	--NIPRVRIEHLNNKKLPISGPLKELQIQTIFHSNSTARIVGVNDFCPTVPKMKSLSY	343	
DG	289	TFNSSSLELDLSYNQLQKTP---PVNTNLNLYLQGNRINEPFISSISFCTVVVDVMNFSL	345	
QY	344	SAISLFNNPVK	354	
DG	346	QVLRLDGNEIK	356	
RESULT	41			
OMD_BOVIN	OMD_BOVIN	STANDARD;	PRT;	422 AA.
AC	O77742;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			


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CC (SLRPS) FAMILY, CLASS II SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X94988; CAA64454.1; -.
DR MGD; MGI:1328364; Fmod.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_Out.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00560; LRR; 9.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00370; LRR; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_Typ; 1.
DR Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal; Sulfation.
FT SIGNAL 1 18
FT CHAIN 19 376
FT DOMAIN 76 92
FT REPEAT 98 117
FT REPEAT 118 141
FT REPEAT 142 167
FT REPEAT 168 188
FT REPEAT 189 212
FT REPEAT 213 235
FT REPEAT 236 256
FT REPEAT 257 280
FT REPEAT 281 305
FT REPEAT 306 325
FT REPEAT 326 355
FT REPEAT 356 376
FT DOMAIN 68 73
FT DISULFID 334 367
FT CARBOHYD 127 127
FT CARBOHYD 166 166
FT CARBOHYD 201 201
FT CARBOHYD 291 291
FT CARBOHYD 341 341
FT SEQUENCE 376 AA; 43054 MW; 45A9EDDB0BADA85B CRC64;
Query Match 16.6%; Score 331; DB 1; Length 376;
Best Local Similarity 29.2%; Pred. No. 5.7e-16;
Matches 90; Conservative 57; Mismatches 131; Indels 30; Gaps 9;
Qy 57 PTRPRSHFPFDLPFCGQCQ---YSRVHCSDLGLFSVPTNPFDPRMLDLQNNKI 113
Dy 69 PPPEPRD-----CPQECDCPPNFTAMYCDNRNKLKLPF-VPSRMKYVYFQNNQI 117
Qy 114 KEIKENDFKGLTSLYGLLNNKLT--KIHPKAFLLTKLRLRYLSHNSQLSEPLNPKS 171
Dy 118 SAIQGVFDNATGLLWALHNGNQITSDKVGKVFSLRHLRLYLDHNNLRMPGLPRS 177
Qy 172 LAELRIENKVKTKQKTFKGMALHVLMSANPLDNNGTEPGAFGV-TVFHIRIAEAK 230
Dy 178 LRELHLHQNISRPNNALEGLNLTALYLLHNEIQEVG---SSMRGLRSLIILDLSYNH 234
Qy 231 LTSVPKGLPPTLLEHLHDYKNISTVELEDFKRYKELQRLGNKNKTIENGSLA----N 286
Dy 235 LRRVPDGLPSALEQYLEHNNVTVPSYFSGPKLLYVRLSHNSLT---NNGLATNTFN 291
Qy 287 IPRVREIHLNNKLLKTPSLGPLKLPYLIQIIFLHSNSTARVGVNDPCTVPKMKKSLYSAI 346
DB 292 SSSLELDLSYNOLQKIP---PVNTINLENLYLQGRINRNEFSISFCTVDDVMNFSKLQVL 348
Qy 347 SLFNNPVK 354
Dy 349 RLIDGNEIK 356
RESULT 45
KERA_CHICK STANDARD; PRT; 353 AA.
AC O42235;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Keratan precursor (KTN) (Keratan sulfate proteoglycan keratocan).
GN KERA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 74-92; 212-220 AND 250-267, AND
RP CARBOHYDRATE-LINKAGE SITES ASN-94; ASN-223 AND ASN-261.
RC TISSUE=Cornea;
RX MEDLINE=98211990; PubMed=9545293;
RA Dunlevy J.R., Neame P.J., Vergnes J.-P., Hassell J.R.;
RT "Identification of the N-linked oligosaccharide sites in chick corneal
RT lumican and keratocan that receive keratan sulfate.";
RL J. Biol. Chem. 273:9615-9621(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20179630; PubMed=10712821;
RA Dunlevy J.R., Beales M.P., Berryhill B.L., Cornuet P.K., Hassell J.R.;
RT "Expression of the keratan sulfate proteoglycans lumican, keratocan
RT and osteoglycin/mimican during chick corneal development.";
RL Exp. Eye Res. 70:349-362(2000).
CC -!- FUNCTION: Play an important role in generating and maintaining a
CC transparent matrix within the corneal stroma.
CC -!- SUBCELLULAR LOCATION: Extracellular matrix.
CC -!- PTM: Binds keratan sulfate chains.
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SLRPS) FAMILY, CLASS II SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF022890; AAC15506.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_Out.
DR Pfam; PF00560; LRR; 8.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00370; LRR; 2.
DR SMART; SM00013; LRRNT; 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 353
FT DOMAIN 43 59
FT REPEAT 65 84
FT REPEAT 85 108
FT REPEAT 109 134
FT REPEAT 135 155
FT REPEAT 156 179
FT REPEAT 180 205

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FT REPEAT 206 226 LRR-S 3.
 FT REPEAT 227 250 LRR-T 5.
 FT REPEAT 251 275 LRR-T 6.
 FT REPEAT 276 295 LRR-S 4.
 FT REPEAT 310 333 LRR-T 7.
 FT REPEAT 334 353 LRR-T 8.
 FT DISULFID 304 344 BY SIMILARITY.
 FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (KERATAN SULFATE).
 FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (KERATAN SULFATE).
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (KERATAN SULFATE).
 FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 353 AA; CBF42601FDF33ED6 CRC64;

 Query Match 16.3%; Score 325; DB 1; Length 353;
 Best Local Similarity 31.4%; Pred. No. 1.4e-15;
 Matches 91; Conservative 50; Mismatches 127; Indels 22; Gaps 10;

 QY 53 NSLFTPREPSHFFPDLFPMCPFCQCQ---YSRVVHCSDLGTSVPTNIPFDTMRMLDLQ 109
 DB 29 NELDP--EHWSH-YTFE---CPQECFCPPSPFNALYCDNKGLEKEIPA-IPARIWYLYLQ 80

 QY 110 NNKIKEIKENDFGKTSYGLIILNNKLTU--IHPKAFLTTKLRLRYLSHNOLSEIPLN 167
 DB 81 NLLIETISEKPFVNATHLRWINLNKNKITNNGIESGVLSKLLRLYLFLEDEEVEVPAP 140

 QY 168 LPKSLAELRIHENKVKTKQDTFGMNAHLVLEMSANPLDNNNGIEPGAEGV-TVFHRI 226
 DB 141 LPVGLQLRLARKNISRIPEGVESNLENLTMLDHQNNLLDSALQSDTFQGLNSLMQLNI 200

 QY 284 LANIPRVREIHLNKKKIPSGLPKYLQIIFLHNSIARVGVNDFCP 333
 DB 260 -FNVSSILDQLSHNQLTKIP---PINAHLEHLHDHNRKSVNGTQICP 305

 RESULT 46
 KERA_COTJA STANDARD; PRT; 353 AA.
 AC Q9DE66;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Keratocan precursor (KTN) (Keratan sulfate proteoglycan keratocan).
 GN KERA.
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Coturnix.
 OX NCBI_TaxID=93934;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cornea, and Sclera;
 RX MEDLINE=20556470; PubMed=11102758;
 RA Corpeuz L.M., Dunlevy J.R., Hassell J.R., Conrad A.H., Conrad G.W.;
 RT "Molecular cloning and relative tissue expression of keratocan and
 RL minican in embryonic quail cornea."
 RL Matrix Biol. 19:693-698(2000).
 CC -!- FUNCTION: Play an important role in generating and maintaining a
 CC transparent matrix within the corneal stroma (By similarity).
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
 CC -!- TISSUE SPECIFICITY: Cornea.
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
 CC (SLRPS) FAMILY. CLASS II SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
 CC -----
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 CC -----
 DR EMBL; AFI28223; AAG48156.1; .
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR003372; LRR_Nterm.
 DR InterPro: IPR003592; LRR_out.
 DR InterPro: IPR003591; LRR_typ.
 DR Pfam; PF00560; LRR; 8.
 DR Pfam; PF01462; LRRNT; 1.
 DR SMART; SM00370; LRR; 2.
 DR SMART; SM00013; LRRNT; 1.
 DR SMART; SM00369; LRR_TYP; 5.
 KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 KW Leucine-rich repeat; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 353 KERATOCAN.
 FT DOMAIN 43 59 CYS-RICH.
 FT REPEAT 65 84 LRR-S 1.
 FT REPEAT 85 108 LRR-T 1.
 FT REPEAT 109 134 LRR-T 2.
 FT REPEAT 135 155 LRR-S 2.
 FT REPEAT 156 179 LRR-T 3.
 FT REPEAT 180 205 LRR-T 4.
 FT REPEAT 206 226 LRR-S 3.
 FT REPEAT 227 250 LRR-T 5.
 FT REPEAT 251 275 LRR-T 6.
 FT REPEAT 276 295 LRR-S 4.
 FT REPEAT 310 333 LRR-T 7.
 FT REPEAT 334 353 LRR-T 8.
 FT DISULFID 304 344 BY SIMILARITY.
 FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (KERATAN SULFATE).
 FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (KERATAN SULFATE).
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (KERATAN SULFATE).
 FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 353 AA; 40279 MW; DEE07614FC598F7D CRC64;

 Query Match 16.3%; Score 325; DB 1; Length 353;
 Best Local Similarity 31.4%; Pred. No. 1.4e-15;
 Matches 91; Conservative 50; Mismatches 127; Indels 22; Gaps 10;

 QY 53 NSLFTPREPSHFFPDLFPMCPFCQCQ---YSRVVHCSDLGTSVPTNIPFDTMRMLDLQ 109
 DB 29 NELDP--EHWSH-YTFE---CPQECFCPPSPFNALYCDNKGLEKEIPA-IPARIWYLYLQ 80

 QY 110 NNKIKEIKENDFGKTSYGLIILNNKLTU--IHPKAFLTTKLRLRYLSHNOLSEIPLN 167
 DB 81 NLLIETISEKPFVNATHLRWINLNKNKITNNGIESGVLSKLLRLYLFLEDEEVEVPAP 140

 QY 168 LPKSLAELRIHENKVKTKQDTFGMNAHLVLEMSANPLDNNNGIEPGAEGV-TVFHRI 226
 DB 141 LPVGLQLRLARKNISRIPEGVESNLENLTMLDHQNNLLDSALQSDTFQGLNSLMQLNI 200

 QY 284 LANIPRVREIHLNKKKIPSGLPKYLQIIFLHNSIARVGVNDFCP 333
 DB 260 -FNVSSILDQLSHNQLTKIP---PINAHLEHLHDHNRKSVNGTQICP 305

 RESULT 47
 FMOD_HUMAN STANDARD; PRT; 376 AA.
 ID FMOD_HUMAN AC Q06828; Q15331;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)

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OM protein - protein search, using sw model

Run on: January 24, 2003, 12:22:00 ; Search time 35 seconds
(without alignments)
2231.196 Million cell updates/sec

Title: US-09-944-457-2

Perfect score: 1992

Sequence: 1 MKEYVLLFLALCSAKPFES.....PATFRCVLSRMSVQLGNFGM 379

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

SPTREMBL_21.*
1: sp.archaea.*
2: sp.bacteria.*
3: sp.fungi.*
4: sp.human.*
5: sp.invertebrate.*
6: sp.mammal.*
7: sp.mhc.*
8: sp.organella.*
9: sp.phage.*
10: sp.plant.*
11: sp.rodent.*
12: sp.virus.*
13: sp.vertibrate.*
14: sp.unclassified.*
15: sp.rvirus.*
16: sp.bacteriap.*
17: sp.archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1118.5	56.1	370	13 Q9DE04	Q9de04 oreochromis
2	968	48.6	187	4 Q9NXP3	Q9npx3 homo sapien
3	950	47.7	359	13 Q9DE03	Q9de03 oreochromis
4	917	46.0	410	13 Q9DDZ7	Q9ddz7 petromyzon
5	915	45.9	310	13 Q9DDZ8	Q9ddz8 petromyzon
6	869.5	43.6	347	13 Q9DE00	Q9de00 petromyzon
7	865.5	43.4	386	13 Q9DDZ9	Q9ddz9 petromyzon
8	638.5	32.1	224	13 Q9DE01	Q9de01 brachydanio
9	520	26.1	108	11 Q9CTL6	Q9ctl6 mus musculus
10	397.5	20.0	699	4 Q94769	Q94769 homo sapien
11	363.5	18.2	674	4 Q8WVA2	Q8wva2 homo sapien
12	354	17.8	120	13 Q9DE02	Q9de02 brachydanio
13	340.5	17.1	796	11 Q9WVC1	Q9wvc1 rattus norv
14	336	16.9	1525	4 Q9Y5Q7	Q9y5q7 homo sapien
15	336	16.9	1529	4 Q94813	Q94813 homo sapien
16	335	16.8	1512	13 Q9DE36	Q9de36 brachydanio

17	332.5	16.7	1440	5 Q20204	Q20204 caenorhabdi
18	331.5	16.6	623	4 Q96K39	Q96k39 homo sapien
19	331.5	16.6	649	4 Q96KB1	Q96kb1 homo sapien
20	331.5	16.6	662	4 Q9P259	Q9p259 mus musculu
21	331.5	16.6	1521	11 Q9R1B9	Q9rlb9 mus musculu
22	331	16.6	1530	13 Q90WZ3	Q90wz3 xenopus lae
23	329	16.5	1521	4 Q95710	Q95710 homo sapien
24	329	16.5	1531	11 Q9WVB5	Q9wvb5 mus musculu
25	328	16.5	1534	4 Q75093	Q75093 homo sapien
26	326	16.4	1504	5 Q9V7F9	Q9v7f9 drosophila
27	325	16.3	1523	11 Q9WVB4	Q9wvb4 mus musculu
28	324	16.3	1480	5 Q9V7F8	Q9v7f8 drosophila
29	324	16.3	1523	11 Q88280	Q88280 rattus norv
30	323	16.2	1531	11 Q88279	Q88279 rattus norv
31	320	16.1	798	4 Q8WWZ2	Q8wwz2 homo sapien
32	320	16.1	1504	5 Q9XIV4	Q9xyv4 drosophila
33	319	16.0	1530	11 Q9WUG5	Q9wug5 rattus norv
34	311.5	15.6	1515	13 Q9DE37	Q9de37 brachydanio
35	309	15.5	1523	4 Q75094	Q75094 homo sapien
36	304.5	15.3	581	6 Q9BGP6	Q9bgp6 macaca fasc
37	304.5	15.3	581	6 Q95KI8	Q95ki8 macaca fasc
38	297.5	14.9	581	4 Q8TF66	Q8tf66 homo sapien
39	296	14.9	1091	11 P70193	P70193 mus musculu
40	289	14.5	1093	4 Q96JA1	Q96ja1 homo sapien
41	289	14.5	1094	4 Q9BYB8	Q9byb8 homo sapien
42	287	14.4	96	11 Q63156	Q63156 rattus norv
43	282.5	14.2	391	11 Q9D3K0	Q9d3k0 mus musculu
44	282.5	14.2	1025	11 Q9Z166	Q9z166 mus musculu
45	282	14.2	1095	13 Q90XG4	Q90xg4 gallus gall
46	281.5	14.1	578	11 Q8R5W3	Q8r5m3 rattus norv
47	281	14.1	542	5 Q9N4G6	Q9n4g6 caenorhabdi
48	276.5	13.9	1513	5 Q9VPF0	Q9vpf0 drosophila
49	276	13.9	603	11 Q70211	Q70211 rattus norv
50	275	13.8	522	4 Q96DN1	Q96dn1 homo sapien

ALIGNMENTS

RESULT 1

Q9DE04 PRELIMINARY; PRT; 370 AA.
ID Q9DE04
AC Q9DE04;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Biglycan-like protein 3.
GN BGL3.

OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidel;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=20496956; PubMed=11040287;
RA Shintani S., Sato A., Toyosawa S., O'Huigin C., Klein J.;
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts.";
RL J. Mol. Evol. 51:363-373(2000).
DR EMBL: AF247821; AAG40156.1; -;
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003592; LRR_Out.
DR InterPro: IPR003591; LRR_tyr.
DR Pfam: PF00560; LRR: 9.
DR Pfam: PF01462; LRRNT: 1.
DR SMART: SM00370; LRR: 2.
DR SMART: SM00013; LRRNT: 1.
DR SMART: SM00369; LRR_TYP: 5.
SQ SEQUENCE 370 AA; 42177 MW; BCD0675694ECA2B7 CRC64;
Query Match 56.1%; Score 1118.5; DB 13; Length 370;

Best Local Similarity 56.7%; Pred. No. 7e-72;

Matches 219; Conservative 52; Mismatches 88; Indels 27; Gaps 4;

QY 1 MKEYVLLFLALCSAKPFSPSHIA--LKN-----MMLKMDTDDDDDDDDDDDDDE 51
DB 1 MRIFLLCLLALGNKPK-YQINVDYLNKNTDKIHEIMISDSNDDDDDDDDDDDDDD 59
QY 52 DNSLPTREPRSHFFPDLFPMCFGCQYSRVHVHSCDGLTSTVPTNIPDTRMLDLQNN 111
DB 60 YND-----EDCPAHCHCSPRVVQCSQDGLISVPDKIPEDTYMIDILQNN 102
QY 112 KIKEIKENDFKGLTSLYGLIINNKLKPIHKPAFLTTKKLRRLYLSHNSQSEIPLNPKS 171
DB 103 DITEIQDQDFGLNKLKYLGLFLINNKRISRIHPKAFKNDNLRLYLSHNSQSEIPLNPKS 162
QY 172 LAELIHNKVKYKQDFKGMNALHVLMSANPLDNNNGTEPGAFEGVTVFHIRIAEAKL 231
DB 163 VIELRFHENQIDRQDAFKGLRKLHVLGELGANPLTNSGIEGAFNGSLTYIGIAEAKL 222
QY 232 TSVKGLPPTLLEHLDYNNKISTVELEDFKRYKELQRLGLGNKNTDIENGSLANIPRVR 291
DB 223 TSIPKDFPSTITSLDYNKISKVEIEDFIRYKNLQRLGLAFNQIKYVENGSLANTPKIR 282
QY 292 EHLNENKLLKIPSGLPKELKYLQIFLHNSIARVGNDFCTVPKMKKSLYSALSIFNN 351
DB 283 EYLDNNRMRKVPGLSLRVLQVIFLHNSIARVGNDFCTVPKMKKSLYSALSIFNN 342
QY 352 PVKYWEMQPATRCVLSRMSVOLGNF 377
DB 343 PVKYWAIQPATRCVTGRRGVOLGNF 368

RESULT 2

Q9NXP3 PRELIMINARY; PRT; 187 AA.

AC Q9NXP3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CDNA FLJ20129 fis, clone COL06190.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK00136; BAA90967.1;
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 3.
SQ SEQUENCE 187 AA; 21074 MW; BDBEE37373CA3DBE CRC64;

Query Match 48.6%; Score 968; DB 4; Length 187;

Best Local Similarity 100.0%; Pred. No. 1.6e-61;

Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 MNALHVLMSANPLDNNNGIEPGAEGVTVFHIRIAEAKLSVPGKLPPTLLEHLDYNNKI 252
DB 1 MNALHVLMSANPLDNNNGIEPGAEGVTVFHIRIAEAKLSVPGKLPPTLLEHLDYNNKI 60
QY 253 STVELEDFKRYKELQRLGLGNKNTDIENGSLANIPRVREIHLNENKLLKIPSGLPKLY 312
DB 61 STVELEDFKRYKELQRLGLGNKNTDIENGSLANIPRVREIHLNENKLLKIPSGLPKLY 120
QY 313 LQIFLHNSIARVGNDFCTVPKMKKSLYSALSIFNNPVPKYWEMQPATRCVLSRMSV 372
DB 121 LQIFLHNSIARVGNDFCTVPKMKKSLYSALSIFNNPVPKYWEMQPATRCVLSRMSV 180

QY 373 QLGNFGM 379

DB 181 QLGNFGM 187

RESULT 3

Q9DE03

ID Q9DE03 PRELIMINARY; PRT; 359 AA.

AC Q9DE03;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Decorin.
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20496956; PubMed=11040287;
RA Shintani S., Sato A., Toyosawa S., O'higin C., Klein J.;
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts."
RL J. Mol. Evol. 51:363-373(2000).
DR EMBL; AF247822; AAG40157.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR00372; LRR Nterm.
DR InterPro; IPR003592; LRR out.
DR InterPro; IPR003591; LRR typ.
DR Pfam; PF00560; LRR; 7.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00370; LRR; 3.
DR SMART; SM00113; LRRNT; 1.
DR SMART; SM00369; LRR typ; 7.
SQ SEQUENCE 359 AA; 39807 MW; F149F9AA4E7572C6 CRC64;

Query Match 47.7%;

Score 950; DB 13; Length 359;

Best Local Similarity 50.8%; Pred. No. 6.7e-60;

Matches 189; Conservative 57; Mismatches 102; Indels 24; Gaps 4;

QY 7 LLFLALCSAKPFSPSHIALKNMMLKMDTDDDDDDDDDDDDNSLFTPREPSRSHFF 66
DB 8 LLVLVACWALPFRQSGFL--DFMM-----EDGSGDPVTEPLP----- 44
QY 67 PFDLFPMPFCQCYSRVHVHSCDGLTSTVPTNIPDTRMLDLQNNKIKEIKENDFKGLTS 126
DB 45 PVIGGPKCFRCQCHLRVLIQCSDLGLKAVPEDIPDDTLLDLQNNKITEIKENDFKNLG 104
QY 127 LYLGLIINNKLKPIHKPAFLTTKKLRRLYLSHNSQSEIPLNPKSLAELRIHNKVKIKQ 186
DB 105 LHALILVNNKLTIIHPKAFSPITKQLRYSKLNLLKEMPANPKSLQELRIHENEITIK 164
QY 187 KDTFKGMNALHVLMSANPLDNNNGTEPGAFEGV-TVFHIRIAEAKLSVPGKLPPTLLE 245
DB 165 KASFGQMSHVIVMELGNSPLKTAGIAGAFADLKRASYIRIADTNITEVPKGLPSLSSEL 224
QY 246 HLDYNNKISTVELEDFKRYKELQRLGLGNKNTDIENGSLANIPRVREIHLNENKLLKIPS 305
DB 225 HLDGNKITTDLTKADRLKMKNAKLGLSYNQISSVENGTLSNAPHLRELHLDNALTYSVP 284
QY 306 GLPELKYLOIIFLHNSIARVGNDFCTVPKMKKSLYSALSIFNNPVPKYWEMQPATRC 365
DB 285 GLPDHKYIQVYLHAKIAAVGTEDFCPPGPNFKKAMYSGLISLFPNVPYWEQVPTFRC 344
QY 366 VLRSRMSVOLGNF 377
DB 345 VFDRSAIQLGNY 356

RESULT 4

Q9DDZ7

ID Q9DDZ7 PRELIMINARY; PRT; 410 AA.

[illegible]

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DR Pfam; PF00560; LRR; 8.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00370; LRR; 4.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_TYP; 6.
FT NON_TER 1
SQ SEQUENCE 347 AA; 38266 MW; 55CC296938CED391 CRC64;

Query Match 43.6%; Score 869.5; DB 13; Length 347;
Best Local Similarity 54.3%; Pred. No. 3.4e-54;
Matches 165; Conservative 54; Mismatches 84; Indels 1; Gaps 1;

QY 74 CPFGQCYSRVVHSCDGLGTSVPTNIPEDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
DB 81 CPFGQCYSRVVHSCDGLGTSVPTNIPEDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 140
QY 134 NKKTKIHPKAFLTTKLRRRLYLSHNLSEIPLNLPKSLAEIRIHENKVKIKQDTPKGM 193
DB 141 NNLIAKIHPKAFAPVWSLDKLYISHNRLTEVPTGIPPSLIELRVHENLIKRVPKDTFINN 200
QY 194 NALHVLMSANPLDNNNGIEPGAFEGV-TVFHIRIAEAKLTSPKGLPPTLLEHLHDYNKI 252
DB 201 GRHLVIELGKNPLPSSGIEVGAENGDKLTVIRISYSKLTQPKLPNSLLEHLEGNEI 260
QY 253 STVELEDFKRYKELORGLGNNKITDIENGSLANIPRVREIHLNENKLLKIPSGLPKLY 312
DB 261 VAIEDLFGPYLFRGLGSYNNKITEVQNGSLAVSGNRLRELHLDNNLLVSPGSLKIRS 320
QY 313 LQITFLHSNSTARVGVNDFCPTVPKMKKSLYSALSIFNNPVKYWEMOPATFCVLSRMSV 372
DB 321 LNVYLHSNKKIKEYKPTDFCPTVSPKRAQYAGISLYDNPVKYWEVPPSFCVHNHNAI 380
QY 373 QLGN 376
DB 381 HFGS 384

RESULT 8
Q9DD29 ID Q9DD29 PRELIMINARY; PRT; 388 AA.
AC Q9DD29;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Biglycan-like protein 1 (Fragment).
GN BGL1.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20496956; PubMed=11040287;
RA Shintani S., Sato A., Toyosawa S., O'hugin C., Klein J.;
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts.";
RL J. Mol. Evol. 51:363-373(2000).
DR EMBL; AF247826; AAG40161.1; -.
DR InterPro; IPR001611; LRR.
DR ZFIN; ZDB-GENE-010102-1; dcn.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00560; LRR; 7.
DR PRINTS; PRO0019; LEURICHRPT.
DR SMART; SM00370; LRR; 5.
DR SMART; SM00369; LRR_TYP; 7.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 347 AA; 38266 MW; 55CC296938CED391 CRC64;

Query Match 43.4%; Score 865.5; DB 13; Length 388;
Best Local Similarity 54.3%; Pred. No. 7.5e-54;
Matches 165; Conservative 53; Mismatches 85; Indels 1; Gaps 1;

QY 74 CPFGQCYSRVVHSCDGLGTSVPTNIPEDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
DB 81 CPFGQCYSRVVHSCDGLGTSVPTNIPEDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 140
QY 134 NKKTKIHPKAFLTTKLRRRLYLSHNLSEIPLNLPKSLAEIRIHENKVKIKQDTPKGM 193
DB 141 NNLIAKIHPKAFAPVWSLDKLYISHNRLTEVPTGIPPSLIELRVHENLIKRVPKDTFINN 200
QY 194 NALHVLMSANPLDNNNGIEPGAFEGV-TVFHIRIAEAKLTSPKGLPPTLLEHLHDYNKI 252
DB 201 GRHLVIELGKNPLPSSGIEVGAENGDKLTVIRISYSKLTQPKLPNSLLEHLEGNEI 260
QY 253 STVELEDFKRYKELORGLGNNKITDIENGSLANIPRVREIHLNENKLLKIPSGLPKLY 312
DB 261 VAIEDLFGPYLFRGLGSYNNKITEVQNGSLAVSGNRLRELHLDNNLLVSPGSLKIRS 320
QY 313 LQITFLHSNSTARVGVNDFCPTVPKMKKSLYSALSIFNNPVKYWEMOPATFCVLSRMSV 372
DB 321 LNVYLHSNKKIKEYKPTDFCPTVSPKRAQYAGISLYDNPVKYWEVPPSFCVHNHNAI 380
QY 373 QLGN 376
DB 381 HFGS 384

RESULT 7
Q9DD29 ID Q9DD29 PRELIMINARY; PRT; 388 AA.
AC Q9DD29;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Biglycan-like protein 1 (Fragment).
GN BGL1.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20496956; PubMed=11040287;
RA Shintani S., Sato A., Toyosawa S., O'hugin C., Klein J.;
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts.";
RL J. Mol. Evol. 51:363-373(2000).
DR EMBL; AF247826; AAG40161.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003592; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00560; LRR; 8.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00370; LRR; 4.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_TYP; 7.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 388 AA; 42542 MW; 2E07169E9BB6071B CRC64;

Query Match 43.4%; Score 865.5; DB 13; Length 388;
Best Local Similarity 54.3%; Pred. No. 7.5e-54;
Matches 165; Conservative 53; Mismatches 85; Indels 1; Gaps 1;

QY 74 CPFGQCYSRVVHSCDGLGTSVPTNIPEDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
DB 81 CPFGQCYSRVVHSCDGLGTSVPTNIPEDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 140
QY 134 NKKTKIHPKAFLTTKLRRRLYLSHNLSEIPLNLPKSLAEIRIHENKVKIKQDTPKGM 193
DB 141 NNLIAKIHPKAFAPVWSLDKLYISHNRLTEVPTGIPPSLIELRVHENLIKRVPKDTFINN 200
QY 194 NALHVLMSANPLDNNNGIEPGAFEGV-TVFHIRIAEAKLTSPKGLPPTLLEHLHDYNKI 252
DB 201 GRHLVIELGKNPLPSSGIEVGAENGDKLTVIRISYSKLTQPKLPNSLLEHLEGNEI 260
QY 253 STVELEDFKRYKELORGLGNNKITDIENGSLANIPRVREIHLNENKLLKIPSGLPKLY 312
DB 261 VAIEDLFGPYLFRGLGSYNNKITEVQNGSLAVSGNRLRELHLDNNLLVSPGSLKIRS 320
QY 313 LQITFLHSNSTARVGVNDFCPTVPKMKKSLYSALSIFNNPVKYWEMOPATFCVLSRMSV 372
DB 321 LNVYLHSNKKIKEYKPTDFCPTVSPKRAQYAGISLYDNPVKYWEVPPSFCVHNHNAI 380
QY 373 QLGN 376
DB 381 HFGS 384

RESULT 8
Q9DE01 ID Q9DE01 PRELIMINARY; PRT; 224 AA.
AC Q9DE01;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Decorin (Fragment).
GN DCN.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20496956; PubMed=11040287;
RA Shintani S., Sato A., Toyosawa S., O'hugin C., Klein J.;
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts.";
RL J. Mol. Evol. 51:363-373(2000).
DR EMBL; AF247824; AAG40159.1; -.
DR ZFIN; ZDB-GENE-010102-1; dcn.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00560; LRR; 7.
DR PRINTS; PRO0019; LEURICHRPT.
DR SMART; SM00370; LRR; 5.
DR SMART; SM00369; LRR_TYP; 7.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 224 AA; 24442 MW; 54A1B7AB91667DF0 CRC64;

Query Match 32.1%; Score 638.5; DB 13; Length 224;
Best Local Similarity 56.5%; Pred. No. 5.6e-38;
Matches 126; Conservative 37; Mismatches 59; Indels 1; Gaps 1;

QY 94 SVPTNIPEDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNKKIKHPKAFLTTKLRR 153
DB 2 TVPEKIPDLDTLLDLQNNKITEIKENDFKGLTSLYGLILNKKIKHPKAFLTTKLRR 61
QY 154 LYLHNSQLSEIPLNLPKSLAEIRIHENKVKIKQDTPKGMNALHVLMSANPLDNNNGIEP 213
DB 62 LYLHNSQLSEIPLNLPKSLAEIRIHENKVKIKQDTPKGMNALHVLMSANPLDNNNGIEP 213
QY 214 GAFEGV-TVFHIRIAEAKLTSPKGLPPTLLEHLHDYNNKISTVELEDFKRYKELORGLG 272
DB 122 GAFADLKRVSATRIADTNLTSTIPKGLPSSLFLHLDGNNKITKVTADSLKGLNLSKLG 181

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QY 169 PKSLAELR---IHENKVKIKQDTPKGMNALHVLMSANP-----LDNGIE 212
D 169 PKSLAELR---IHENKVKIKQDTPKGMNALHVLMSANP-----LDNGIE 212
Db 396 FQDLHNLNLLSYDNKLTQVAKGTFSAIRAIQTMHLAQNPFICDCHLKWLDYLTNPTE 455
QY 213 -PGA-----FEGVTVFH 223
Db 456 TSGARCTSPRLANKRIGQIKSKKFCSTEDYRSKLSGDCFDADLACPEKRCGGTV-- 513
QY 224 IRIAEAKLTSPKGLPPTLLEHLHDYKISTVELED-FKRYKELQRLGLGNKNTIDIEG 282
Db 514 -DCSNQKLNKIPHIPOYTAELRNNEFTVLEATGIFKFLPQLRKINLNKNTIDIEG 572
QY 283 SLANIPIVREIHLNENKLNK-----KIPSGLPKLYLIQIFLHNSIARVGVNDFCPTVPM 338
Db 573 AFEAGSGVNEILLTSNRLENVQHKMFGLSKTL---MLRNSRICVGNDSFTGLGVR 629
QY 339 KKSILY-----SAISLFPNPVKYWMOPATFRC-----VLSRMS 371
Db 630 LLSLYDNQITTVAPGAFGLHLSLSTLNLIANP-----FNCNCHLAWLGEWLRRKR 679
QY 372 VOLGN 376
Db 680 IVTGN 684

RESULT 14
QY507
ID QY507 PRELIMINARY; PRT; 1525 AA.
AC QY507;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE SLIT2.
GN SLIT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=99200389; PubMed=10102266;
RA Wang K.H., Brose K., Arnott D., Kidd T., Goodman C.S., Henzel W.,
RA Tessier-Lavigne M., Kidd T.;
RT "Purification of an axon elongation- and branch-promoting activity
RT from brain identifies a mammalian Slit protein as a positive regulator
RT of sensory axon growth."
RL Cell 96:771-784(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=99200391; PubMed=10102268;
RA Brose K., Bland K.S., Wang K.H., Arnott D., Henzel W., Goodman C.S.,
RA Tessier-Lavigne M., Kidd T.;
RT "Slit proteins bind Robo receptors and have an evolutionarily
RT conserved role in repulsive axon guidance."
RL EMBL; AF133270; AAD25539.1; -.
DR HSSP; P00743; ICCF.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR003645; FOLN.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00008; EGF; 9.
DR Pfam; PF00054; laminin_G; 1.
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DR Pfam; PF00560; LRR; 17.
DR Pfam; PF01463; LRRCT; 4.
DR Pfam; PF01462; LRRNT; 4.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00001; EGF_like; 7.
DR SMART; SM00274; FOLN; 2.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00370; LRR; 6.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_TYP; 8.
DR PROSITE; PS00101; ASX_HYDROXYL; UNKNOWN_2.
DR PROSITE; PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_9.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS01187; EGF_CA; 2.
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SQ SEQUENCE 1525 AA; 169394 MW; 8A81CDE34EF06A73 CRC64;

Query Match 16.9%; Score 336; DB 4; Length 1525;
Best Local Similarity 26.5%; Pred. No. 1.9e-15;
Matches 105; Conservative 61; Mismatches 120; Indels 110; Gaps 12;

QY 74 CPFGCQCYRVVHCSDGLTSVPTNIPDFT-----RMLDL 108
D 74 CPFGCQCYRVVHCSDGLTSVPTNIPDFT-----RMLDL 108
Db 277 CPAACTCSNNIVDCRGKLTETIPNLP-ETITEIRLEONTIKVPPGAFSPYKLRIDL 335
QY 109 QNNKIKEIKENDFKGLTSLYGLILNKKLTAKHFKAFETTKKLRRLYLHNSQLSEIPLNL 168
D 109 QNNKIKEIKENDFKGLTSLYGLILNKKLTAKHFKAFETTKKLRRLYLHNSQLSEIPLNL 168
Db 336 SNNQISELAPDAFQGLRSLNLSLVYGNKITELPKSLPEGLSLQLLLNANKINCLRVDA 395
QY 169 PKSLAELR---IHENKVKIKQDTPKGMNALHVLMSANP-----LDNGIE 212
D 169 PKSLAELR---IHENKVKIKQDTPKGMNALHVLMSANP-----LDNGIE 212
Db 396 FQDLHNLNLLSYDNKLTQIAKGTFSPLRAIQTMHLAQNPFICDCHLKWLDYLTNPTE 455
QY 213 -PGA-----FEGVTVFH 223
D 213 -PGA-----FEGVTVFH 223
Db 456 TSGARCTSPRLANKRIGQIKSKKFCSTEDYRSKLSGDCFDADLACPEKRCGGTV-- 513
QY 224 IRIAEAKLTSPKGLPPTLLEHLHDYKISTVELED-FKRYKELQRLGLGNKNTIDIEG 282
D 224 IRIAEAKLTSPKGLPPTLLEHLHDYKISTVELED-FKRYKELQRLGLGNKNTIDIEG 282
Db 514 -DCSNQKLNKIPHIPOYTAELRNNEFTVLEATGIFKFLPQLRKINLNKNTIDIEG 572
QY 283 SLANIPIVREIHLNENKLNK-----KIPSGLPKLYLIQIFLHNSIARVGVNDFCPTVPM 338
D 283 SLANIPIVREIHLNENKLNK-----KIPSGLPKLYLIQIFLHNSIARVGVNDFCPTVPM 338
Db 573 AFEAGSGVNEILLTSNRLENVQHKMFGLSKTL---MLRNSRICVGNDSF-----I 623
QY 339 KKSILY-----SAISLFPNPVKYWMOPATFRCVLSRMSVOL 374
D 339 KKSILY-----SAISLFPNPVKYWMOPATFRCVLSRMSVOL 374
Db 624 GLSSVRLSLSYDNQIT--TVAPGAFDTLHLSLSTLNL 657

RESULT 15
QY4813
ID QY4813 PRELIMINARY; PRT; 1529 AA.
AC QY4813;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Slit-2 protein.
GN Slit-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99033071; PubMed=9813312;
RA Itoh A., Miyabayashi T., Ohno M., Sakano S.;
RT "Cloning and expressions of three mammalian homologues of drosophila
RT slit suggest possible roles for slit in the formation and maintenance
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RT of the nervous system."
RL Brain Res. Mol. Brain Res. 62:175-186(1998).
DR EMBL: AB017168; BAA35185.1; -.
DR HSP; P00743; 1CGF
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR003645; FOLN.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_Lyp.
DR Pfam; PF00008; EGF; 9.
DR Pfam; PF00054; laminin_G; 1.
DR Pfam; PF00560; LRR; 17.
DR Pfam; PF01463; LRRCT; 4.
DR Pfam; PF01462; LRRNT; 4.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_Ca; 2.
DR SMART; SM00001; EGF_like; 7.
DR SMART; SM00274; FOLN; 2.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00370; LRR; 6.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_Typ; 8.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
DR PROSITE; PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_9.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS01187; EGF_Ca; 2.
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SQ SEQUENCE 1529 AA; 169866 MW; 5D19CC5E7FD461BA CRC64;

Query Match 16.9%; Score 336; DB 4; Length 1529;
Best Local Similarity 26.0%; Pred. No. 1.9e-15;
Matches 105; Conservative 61; Mismatches 120; Indels 118; Gaps 12;
QY 74 CPGGQCYSRVVHCSDLGTSVPTNPFDT-----RMLDL 108
DB 273 CAACTCSNNIVDCRGKGLTEIPTNLP-ETITEIRLEQNTIKVPPGAFSPYKKLRIDL 331
QY 109 QNNKIKEKENDFKGLTSLYGLILNNKLTTHPKAFLTTKKRLYLHSHNQLSEIPLNL 168
DB 332 SNNQISELAPDAFQGLRSLSLVLYGNKITEPKSLFGLFSLQLLLNANKINCLRVA 391
QY 169 PKSLAELR---IHENKVKKIQKDTFGMNAHLVLEMSANP-----LDNNGIE 212
DB 392 FQDLHNLNLLSYDNKLTQIAKGTFSPLRAIQTHLAQNPFICDCHLKLWADLYLHTNP 451
QY 213 -----PGA----- 215
DB 452 TSGARCTSPRIANRRIQIKSKFRCSAKQYFIPGTYRSLSGDCFADLACPEKCR 511
QY 216 FGVVVFHRIAEAKLTSPVGLPPTLLEHLDYKNTISTVELED-FKRYKELQRLGLGN 274
DB 512 CGTTV---DCSNQKLNKIPHIPOYTAELRLNNEFTVLEATGIFKKLPOLRKINFSNN 568
QY 275 KITDIENGLANIPRVRIHLENNKLK----KIPSGPELKYLIIFLHNSIARVGVND 330
DB 569 KITDIEGAFEGACSGVNEILLTSNRLENVQHKMFKGLSESLTL---MLRSNRITCVGNS 625
QY 331 FCPPTVPMKKSLSYSAISLFPNPKVWQEPATFRCVLSRMSVOL 374
DB 626 F-----IGLSVRLSLYDNOIT--TVAPGAFDTLHSLSTLN 661
RESULT 16

Q9DE36

ID Q9DE36 PRELIMINARY; PRT; 1512 AA.
AC Q9DE36;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE SLIT2.
GN SLIT2.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MICHIGAN;
RA Yeo S.Y.; Okamoto H.;
RT "zebrafish slit2 homolog."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF210321; AAG36773.1; -.
DR HSP; P00740; 1EDM.
DR ZFIN: ZDB-GENE-010306-3; slit2.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR003645; FOLN.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00008; EGF; 9.
DR Pfam; PF00054; laminin_G; 1.
DR Pfam; PF00560; LRR; 18.
DR Pfam; PF01463; LRRCT; 4.
DR Pfam; PF01462; LRRNT; 4.
DR PRINTS; PRO0010; EGF_BLOOD.
DR PRINTS; PRO0011; EGF_LAMININ.
DR PRINTS; PRO0019; LEURICHRPT.
DR SMART; SM00041; CT; 1.
DR SMART; SM00181; EGF; 9.
DR SMART; SM00179; EGF_Ca; 9.
DR SMART; SM00001; EGF_like; 6.
DR SMART; SM00274; FOLN; 2.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00370; LRR; 14.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_Typ; 17.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_9.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS01187; EGF_Ca; 2.
SQ SEQUENCE 1512 AA; 166669 MW; 60888C0AF0C3D630 CRC64;

Query Match 16.8%; Score 335; DB 13; Length 1512;
Best Local Similarity 27.1%; Pred. No. 2.2e-15;
Matches 110; Conservative 61; Mismatches 129; Indels 106; Gaps 12;
QY 61 PRSHFFPDLFPMCPGCGCYSRVVHCSDLGTSVPTNPFDT----- 103
DB 253 PQSHSSCSVL--OCPELCTCSNNVDCRGKGLTEIPTNLP-ETITEIRLEQNSIKIIPAG 309
QY 104 -----RMLDLQNNKIKEKENDFKGLTSLYGLILNNKLTTHPKAFLTTKKLRRLY 155
DB 310 AFAPYKRLRRIDLNNQITELASDSFQGLRSLSLVLYGNKITEPKLGLFDGLFSLQLLL 369

Query Match	16.7%	Score 332.5;	DB 5;	Length 1440;
Best Local Similarity	26.5%;	Pred. No. 3.1e-15;		
Matches 108; Conservative	57;	Mismatches 126;	Indels 117;	Gaps

Qy	74	CPFCQCYSRVHSGDGLGTSVTNPIDFDRMLDQNNKIKETKENDFKGLTSLYGLILN	133
Db	17	CPAECVCVDRTVSCVCGOOLTEVPQNPINDIIRLDQDNEITKGPNDFFSSLMNLKALQLM	76
Qy	134	NNKUTKTHPKAFUTTKKLRLRYLSHNOLSEIPNLNPKS---LAELRIHENKVKKIQKDTF	190
Db	77	DNQIVTHNQSFSSLVFLQKLRLSRNRIRHLPDNVFQNNLKLTHLDSENDITVWSDAQL	136
Qy	191	KGMNALHVLEMSANP---LDNNGI-----EP--GAFGEVTVFVH--	223
Db	137	QGPEFLEVLNLDKNHIFCLENNVTSWVSLEVLTLNGNRLTTFEEPSNARFOLDLFNPP	196
Qy	224	-----IIRIAEAK-----	230
Db	197	WNCDRLRWKWKLEKAEAGQNKTVCAPLNQLQSSSEIILQDKFTWCSGNKRKRYKKTCT	256
Qy	231	-----LTSVPKGLPPTLELHLNDYKTKSTVELEDFKRYKELQRL	269
Db	257	AETCPLECTGTTCVDCRDSGLIYVVTNLPSPSTEIRLEQNLSSISPSFKMLKMLTRL	316
Qy	270	GLGNKTKTDIENGSLANIPRVRIEHLNENKMKKIPSGLPE--KLYLQIIFLHNSIA--RV	326
Db	317	DLSKNIITEIQPAFLGLHNLHTLVLYGNNITDLKSDTFEGLSGIQLLLLLNANQLTCIRR	376
Qy	327	GVNDFCETVPKMKKSLYSATSLFNNPVKYYWEMQPAATFCVLRMSVQL	374
Db	377	GTDFH---VPKL-----SMLSYLNDNIK--SISVTFONLTSLSLTHL	44

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RESULT 18
Q96K39
ID Q96K39 PRELIMINARY; PRT; 623 AA.
AC Q96K39;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CDNA FLJ14788 fis, clone NT2RP4000925, weakly similar to fibromodulin
DE precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RX [1]
SEQUENCE FROM N.A.
RA Isegai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Matsunawa H., Ishii S., Kawai Y., Saico K., Yamamoto J., Wakamatsu A.
RA Nakamura Y., Nagahari K., Masuno Y., Sasaki N.;
RA "NEDO human cDNA sequencing project."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RT EMBL; AK027694; BAB55303.1; -.
DR InterPro; IPR003961; FN.III.

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Best Local Similarity 33.08; Pred. No. 1.4e-15;
Matches 86; Conservative 37; Mismatches 111; Indels 27; Gaps 5;

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QY 74 CPFGCOCYGRVYHCSDLGITSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLIIN 133
Db 44 CFSVCRCDAFYICNDRELTSIPTGIPEDATTLYLQNNQI-----N 84

QY 134 NKKLTAKHPKAFLTATTKLRRRLYLSHNOLSEIPLNPKSLAELRIHENKYVKTKQDFTFGM 193
Db 85 NAGI-----PSDLKNLKVERIYLVHNSLDEFPNTNPKYVKELHQLQENNTITVYDSLKI 140

QY 194 NALHVLEMSANPLDNNGTGPGAFGCVTVFHIR-IAEAKLTSYKPGILPTLLELHLDYNKI 252
Db 141 PYLEELHLDNNSVSAVSTEAGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDNNRI 200

QY 253 STVELEDFFKRYKELQRLGLGNKTKTDIENG--LANIPRVRETHLENNKLKKTSPGLPEL 310
Db 201 STISSPSLOGLTSLKRLVLDGNLNNHGLGDKVFNNLVNLTSLVRSNLTAAPVNLPGT 260

QY 311 KYLQIIFLHSNSIARGVYNDF 331
Db 261 N-LRKLYLDNHNIRVPPNAF 280

RESULT 21
Q9RIB9
ID Q9RIB9 PRELIMINARY; PRT; 1521 AA.
AC Q9RIB9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE SLIT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS WEBSTER/ICR;
RX MEDLINE=99365246; PubMed=10433822;
RA Yuan W., Zhou L., Chen J.H., Wu J.Y., Rao Y., Ornitz D.M.;
RT "The mouse SLIT family: secreted ligands for ROBO expressed in
RL Dev. Biol. 212:290-306(1999).
DR EMBL: AF144628; AAD44759.1; -.
DR HSSP: P00743; ICCF.
DR MGD; MGI:1315205; Slit2.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR003645; FOLN.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00008; EGF; 9.
DR Pfam; PF00054; laminin_G; 1.
DR Pfam; PF00560; LRR; 17.
DR Pfam; PF01463; LRRCT; 4.
DR Pfam; PF01462; LRRNT; 4.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00001; EGF_like; 7.
DR SMART; SM00274; FOLN; 2.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00370; LRR; 6.
DR SMART; SM00082; LRRCT; 4.

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DR EMBL; AY046070; AAL02123.1; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR Pfam; PF00008; EGF_9.
DR Pfam; PF00054; laminin_G; 1.
DR Pfam; PF00560; LRR; 17.
DR Pfam; PF01463; LRRCT; 4.
DR PROSITE; PS00185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_9.
DR PROSITE; PS01186; EGF_2; UNKNOWN_7.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_2.
SQ SEQUENCE 1530 AA; 170101 MW; AB4C4650CBA4218C CRC64;

Query Match 16.68; Score 331; DB 13; Length 1530;
Best Local Similarity 26.88; Pred. No. 4.3e-15;
Matches 106; Conservative 60; Mismatches 120; Indels 110; Gaps 12;

Qy 74 CPFGCCYRVVHCSDLGTSVPTNIPFDT-----RMLDL 108
Db 282 CPAACTCSNNIVDCRGKGLTEIPTNLP-ETITEMRLQNSIKVIPPGAFSPYKLLRRIDL 340

Qy 109 QNNKIKEIKENDFKGLTSLYGLILNNKLTAKIHPKAFLTTRKLRRLYLHNSQLSEIPLNL 168
Db 341 SNNQISELAPDAFOGLRSLNSLVLYGNKITELPKLFEGLFSQLQLLLNANKINCLRVDS 400

Qy 169 PKSLAELR---IHENKVKKIQKDTFGKMNALHVLMSANP-----LDNNGIE 212
Db 401 FQDLHNLNLLSLYDNKLTQIAKGTSPRLAQTQIHLAQNPFICDCHLKLADYLHTNP 460

Qy 213 -PGA-----FEQVTVFH 223
Db 461 TSGARCTSPRLANKRIGQIKSKFRCSGTEDYRSKLSGDCFADLACPEKCRCEGTVV-- 518

Qy 224 IRIAEAKLTSVPKGLPPTLLLEHLNDYKNISTVELED-FKRYKELQRLGLGNKNTIDENG 282
Db 519 -DCSNQKLTTPIDHPQYTAELRLNNEFTVLEATGIFKKLPQLRKINLSNNKITDIEG 577

Qy 283 SLANIPRVREIHLNENKLLK---KIPSGLPKLYLQIIFLHNSIARVGVNDFCPTVPKM 338
Db 578 AFEAGANGVNEILLTSNRLENVQHMKFGLEKPLAQTQIHLAQNPFICDCHLKLADYLHTNP 630

Qy 339 KKSLSAISLFFNNPVKYMOPATFRCLVSRMSVOL 374
Db 631 --SSVRLSLYDNQIT--TVAPGAFDTLHLSLSTLNL 662

RESULT 23
O95710 PRELIMINARY; PRT; 1521 AA.
AC O95710;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Neurogenic extracellular SLIT protein SLIT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY, AND BRAIN;
RX MEDLINE=99279238; PubMed=10349621;
RA Holmes G.P., Negus K., Burridge L., Raman S., Algar E., Yamada T.,
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RA Little M.H.;
RT "Distinct but overlapping expression patterns of two vertebrate slit
RT homologs implies functional roles in CNS development and
RT organogenesis.";
RL Mech. Dev. 79:57-72(1998).
DR EMBL; AF055585; AAD04309.1; -.
DR HSSP; P00743; ICCF.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR Pfam; PF00008; EGF; 9.
DR Pfam; PF00054; laminin_G; 1.
DR Pfam; PF00560; LRR; 17.
DR Pfam; PF01463; LRRCT; 4.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00001; EGF_Like; 7.
DR SMART; SM00274; FOLN; 2.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00370; LRR; 5.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_TYP; 8.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
DR PROSITE; PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_9.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS01187; EGF_CA; 2.
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SQ SEQUENCE 1521 AA; 168947 MW; C05A0DFD7D78C48C9 CRC64;

Query Match 16.5%; Score 329; DB 4; Length 1521;
Best Local Similarity 25.7%; Pred. No. 5.9e-15;
Matches 101; Conservative 64; Mismatches 124; Indels 104; Gaps 11;

Qy 74 CPFGCCYRVVHCSDLGTSVPTNIPFDT-----RMLDL 108
Db 273 CPAACTCSNNIVDCRGKGLTEIPTNLP-ETITEIRLEQNTIKVIPPGAFSPYKLLRRIDL 331

Qy 109 QNNKIKEIKENDFKGLTSLYGLILNNKLTAKIHPKAFLTTRKLRRLYLHNSQLSEIPLNL 168
Db 332 SNNQISELAPDAFOGLRSLNSLVLYGNKITELPKSLFEGLSLQLLLNANKINCLRVDA 391

Qy 169 PKSLAELR---IHENKVKKIQKDTFGKMNALHVLMSANP-----LDNNGIE 212
Db 392 FQDLHNLNLLSLYDNKLTQIAKGTSPRLAQTQIHLAQNPFICDCHLKLADYLHTNP 451

Qy 213 -PGA-----FEQVTVFH 223
Db 452 TSGARCTSPRLANKRIGQIKSKFRCSGTEDYRSKLSGDCFADLACPEKCRCEGTVV-- 509

Qy 224 IRIAEAKLTSVPKGLPPTLLLEHLNDYKNISTVELED-FKRYKELQRLGLGNKNTIDENG 282
Db 510 -DCSNQKLTTPIDHPQYTAELRLNNEFTVLEATGIFKKLPQLRKINLSNNKITDIEG 568

Qy 283 SLANIPRVREIHLNENKLLKIPSGL-PEKLYLQIIFLHNSIARVGVNDFCPTVPKMK 341
Db 569 AFEAGANGVNEILLTSNRLENVQHMKFGLEKPLAQTQIHLAQNPFICDCHLKLADYLHTNP 622

Qy 342 LYSATSLFNNPVKYMOPATFRCLVSRMSVOL 374
Db 623 SVRMLSLYDNQIT--TVAPGAFDTLHLSLSTLNL 653
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RESULT 24
Q9WVB5 PRELIMINARY; PRT; 1531 AA.
ID Q9WVB5
AC Q9WVB5
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SLIT1.
GN SLIT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS WEBSTER/ICR;
RX MEDLINE=99365246; PubMed=10433822;
RA Yuan W., Zhou L., Chen J.H., Wu J.Y., Rao Y., Ornitz D.M.;
RT "The mouse SLIT family: secreted ligands for ROBO expressed in
RL Dev. Biol. 212:290-306(1999).
DR EMBL; AF144627; AAD44758.1; -.
DR HSSP; P00743; ICCF.
DR MGD; MGI:1315203; Slit1.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR003645; FOLN.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR00372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00008; EGF; 9.
DR Pfam; PF00054; laminin_G; 1.
DR Pfam; PF00560; LRR; 19.
DR Pfam; PF00560; LRR; 19.
DR Pfam; PF01463; LRRCT; 4.
DR PRINTS; P000041; CT; 1.
DR SMART; SM00010; EGF_BLOOD.
DR SMART; SM000179; EGF_CA; 2.
DR SMART; SM00001; EGF_like; 7.
DR SMART; SM00274; FOLN; 2.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00370; LRR; 3.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_TYP; 10.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
DR PROSITE; PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_9.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS01187; EGF_CA; 2.
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SQ SEQUENCE 1531 AA; 167546 MW; F7D09AA6693A4F30 CRC64;

Query Match 16.5%; Score 329; DB 11; Length 1531;
Best Local Similarity 25.5%; Pred. No. 6e-15;
Matches 100; Conservative 62; Mismatches 116; Indels 114; Gaps 10;

QY 74 CPFCQCYSRVHVCSDGLGLSVPTNPDPD-----RMLDL 108
Db 282 CPAMCSCSGIVDCRGKGLTAIPANLP-ETWTEIRLELNGIKSIIPGAFSPYKLRIDL 340
QY 109 QNNKIKEIKENDFKLTLGLIINNNKLTIIHPKAFLTITTKLRLRYLSNOLSEI---P 165

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Db 73 CPRVCSCTGLNVDCHSHRGLTSVPRKISADVERLELQGNLTVIYETDFQRLTKLRMLQLT 132
QY 134 NNLTKIHPKAFLLTKRLRLYLSHNQLSEIPLNL---PKSLAELRHENKVKKIQKDTF 190
Db 133 DNQIHTIERNFQDVLUSLRANRLNKAIPENFVTSASLLRLDISNNVITTVGRVF 192
QY 191 KGMALHVLNSANPLDNGI---EPGAFEGVTVFHI----- 224
Db 193 KGAQSLRSIQ-----LDNNQITCLDEHAFGLVELEILTNNNLTSILPHNIFGGLRLR 247
QY 225 -----RIA----- 227
Db 248 ALRLSDNPFACDCHLSWLSRSLRATRLAPYTRCQSPSQLKGONVADLHDQFKCSGLTE 307
QY 228 -----EAKLTSVPKGLPPTLLELHLDYKNKISTVELEDFK 261
Db 308 HAPMECGAENSCPHPCRCADGIVCREKSLTSVPTLPDDTTELRLEQNFITELPPKSF 367
QY 262 RYKQLRLGLGNKITTIDENGLANIPRVREIHLNENKLLKIPSGL-PELKYLQIIFLHS 320
Db 368 SFERLRRLDLSNNISRLTAHDALSQKQLTTLVLYGNKIKRDLPSGVFKGLSLQLLLNA 427
QY 321 NSIARVGVNDPCPTVPKMKSLY---SAISLNNPVKYWMQPATFRCVLSRMSVOL 374
Db 428 NEISCIRKDAF-----RDLHSLSLSLYDNNIQ--SLANGTFDAMKSIKTVHL 473

RESULT 27
Q9WB4 PRELIMINARY; PRT; 1523 AA.
AC Q9WB4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SLIT3 (Fragment).
GN SLIT3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS WEBSTER/ICR;
RX MEDLINE=95365246; PubMed=10433822;
RA Yuan W., Zhou L., Chen J.H., Wu J.Y., Rao Y., Ornitz D.M.;
RT "The mouse Slit family: secreted ligands for ROBO expressed in
RL patterns that suggest a role in morphogenesis and axon guidance.";
RL Dev. Biol. 212:290-306(1999).
DR EMBL; AF144629; AAD44760.1; -.
DR HSSP; P01132; 1EGF.
DR MGD; MGI:1315202; Slit3.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF-II.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_Out.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00008; EGF; 9.
DR Pfam; PF00054; laminin_G; 1.
DR Pfam; PF00560; LRR; 19.
DR Pfam; PF01463; LRRCT; 4.
DR Pfam; PF01462; LRRNT; 4.
DR PRINTS; PR00010; EGFBLLOOD.
DR PRINTS; PR00011; EGFFLAMININ.
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DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 5.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00370; LRR; 7.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_Typ; 7.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
DR PROSITE; PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_9.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS01187; EGF_CA; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
FT NON_TER 1523 1523
SQ SEQUENCE 1523 AA; 167711 MW; F43A3F3E016C4BFC CRC64;

Query Match 16.3%; Score 325; DB 11; Length 1523;
Best Local Similarity 25.4%; Pred. No. 1.1e-14;
Matches 100; Conservative 59; Mismatches 111; Indels 124; Gaps 9;

QY 74 CPGCCQCYSRVHCHSDGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
Db 34 CPTKCTCSAASVDCHGLRAVPRGIPRANERLDLDNRNITRTKMDFAGLNLRVHLE 93
QY 134 NNLTKIHPKAFLLTKRLRLYLSHNQLSEIPLNLPS---LAELRIHENKVKKIQKDTF 190
Db 94 DNOVSTIERGAFQDLKQLERLRNKNKQLVPELLFQSTPKLTRDLSENQIGIPRKAF 153
QY 191 KGMALHVLNSANPLDNG--IEGAREG-----VTVF----- 222
Db 154 RGVTVGNLQ-----LDNNHISCIEDGAPRALRDLLEILTNNNNISRLVTSFNHMPKIR 208
QY 223 -----HIR-----IAEK----- 230
Db 209 TLRHLSNHYLCHDLAWLSDWLQRRTIGOTLCMAPVHLRGFSVADVOKKEVCPGPHS 268
QY 231 -----LTSVPKGLPPTLLELHLDYKNKISTVELEDFK 261
Db 269 EAPACNANSLSCPSACSCSNIVDCRGKGLTEIPANLPEGIVEIRLEQNSIKSIPAGFT 328
QY 262 RYKELORLGLGNKITTIDENGLANIPRVREIHLNENKLLKIPSGLPE-LKYLIQIIFLHS 320
Db 329 QYKLRIDISKNQISDIAPDAFQGLKSLTSVLYGNKITEIPKGLDGLVSLQLLLNA 388
QY 321 NSIARVGVNDPCPTVPKMKSLYSALSFNPNVK 354
Db 389 NKINCLRVNTF-----QDLQNLNLLSYDNKLQ 416

RESULT 28
Q9V7F8 PRELIMINARY; PRT; 1480 AA.
AC Q9V7F8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE SLI protein.
GN SLI OR CG8355.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
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DR Pfam; PF00560; LRR; 19.
DR Pfam; PF01463; LRRCT; 4.
DR Pfam; PF01462; LRRNT; 4.
DR PRINTS; PR00438; GFCYSKNOT.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_Like; 8.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00370; LRR; 5.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_TYP; 9.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
DR PROSITE; PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_9.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS01187; EGF_CA; 2.
DR Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
KW SEQUENCE 1523 AA; 167767 MW; 6CE1B7AF9244478E CRC64;

Query Match 16.3%; Score 324; DB 11; Length 1523;
Best Local Similarity 25.4%; Pred. No. 1.3e-14;
Matches 100; Conservative 59; Mismatches 111; Indels 124; Gaps 9;

QY 74 CPFGCCYSRVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKETKENDFKGLTSLYGLILN 133
DB 34 CPTKCTSAASVDCGGLGLRAVPRGIPRNERLDLDRNTRITKMDFTGLKNLRVLHLE 93

QY 134 NKKITKHPKAFITTKLRLYLSHNOLSEIPLNPKS---LAELRIHENKVKKIQKDTF 190
DB 94 DNQSVTERGAFQDLKQLERLRLNKNLQVLPPELLFQSTPKLTLDELSENIQIIPKAF 153

QY 191 KGMALHVLANSAPLDNNG---LEPAFEG-----VTVF----- 222
DB 154 RGVTVGNLQ-----LDNNHISCIEDGAFRALRDLLEILTNNNNISRLVTSFNHPKIR 208

QY 223 -----HIR---IAEK----- 230
DB 209 TLRHSHLYCDCHLAWLSDWLRORRTIGQFTLCMAVPHLRGVSADVQKEVCPGPHS 268

QY 231 -----LTSVPKGLPPTLLEHLHDYNNKISTVELEDFK 261
DB 269 EAPACNANSLCPSACSCSNVDCRGKGLTEIPANLPPEGIVEIRLEQNSIKSPAGAFI 328

QY 262 RYKELQRLGLGNKTTIDENCSLANIPRVREIHLNKKIKIPSGLPE-LKYLIQIFLHS 320
DB 329 QYKKLRIDISKQISDIADPAFGKLSLTSVLYGNKITEIPKGLFDGLVSLQLLLNA 388

QY 321 NSIARVGVNDFCTVPRMKKSLYSALSFNNPVK 354
DB 389 NKINCLRVNTF-----QDLQNLNLSLYDNKLQ 416

RESULT 30
O88279 PRELIMINARY; PRT; 1531 AA.
AC O88279;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MEGF4.
GN MEGF4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE=98360089; PubMed=9693030;
RA Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
RT *Identification of high-molecular-weight proteins with multiple EGF-
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RT like motifs by motif-trap screening."
RL Genomics 51:27-34(1998).
DR EMBL; AB011530; BAA32460.1; -.
DR HSSP; P00743; IAPO.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000561; EGF-Like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR003645; FOLN.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Nterm.
DR InterPro; IPR000372; LRR_Oterm.
DR InterPro; IPR003592; LRR_Out.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00008; EGF; 9.
DR Pfam; PF00054; laminin_G; 1.
DR Pfam; PF00560; LRR; 19.
DR Pfam; PF01463; LRRCT; 4.
DR Pfam; PF01462; LRRNT; 4.
DR PRINTS; PR00010; EGF_BLOOD.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00001; EGF_Like; 7.
DR SMART; SM00274; FOLN; 3.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00370; LRR; 3.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_TYP; 10.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
DR PROSITE; PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_9.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS01187; EGF_CA; 2.
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SQ SEQUENCE 1531 AA; 167497 MW; DFC4B60CCBC5529A CRC64;

Query Match 16.2%; Score 323; DB 11; Length 1531;
Best Local Similarity 25.0%; Pred. No. 1.6e-14;
Matches 98; Conservative 64; Mismatches 116; Indels 114; Gaps 10;

QY 74 CPFGCCYSRVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKETKENDFKGLTSLYGLILN 108
DB 282 CPAMCSCSNGIVDCRGKGLTAIPANLP-ETMTETIRLELNGIKSIPPGAFSPYKLRIDL 340

QY 109 QNNKIKETKENDFKGLTSLYGLITLNNKLTTHKRAFLTKLRLYLSHNOLSEI---P 165
DB 341 SNNQIAETAPDAFQGLRLSNLSLVYGNKTTDLPRGVFGGLYTLQLLLNANKINCIRPDA 400

QY 166 LNLPSKLAELRIHENKVKKIQKDTFKGMNALHVLANSAP-----LDNNGIE 212
DB 401 FQDLQNLNLSLYDNKIQSLAKGTTSLRAIQTLLHAQNPFTCDCLNKLWDLFLRTNPTE 460

QY 213 -PGA-----PEGVTVFH----- 223
DB 461 TTGARCASPRRLANKRIGQIKSKKFCRCAKEQYFIPGTEDYHLNSETSDVACPDKCRE 520

QY 224 ---IRIAEAKLTSPKGLPPTLLEHLHDYNNKISTVELED-FKRYKELQRLGLGNKTTDI 279
DB 521 ASVVECSGLKSLKIPERIPQSTTELELNNEISILEATGLFKLSHLKINLSNNKVSIEI 580

QY 280 ENGLANIPRVREIHLNKKIKIPSGL-PELKYLIQIFLHNSIARVGVNDFCTVPRK 338
DB 581 EDGTFEGATSVSELHLTANQLESVRSGMFRGLDGLRTLMLRNNRISCIHDSFTGLRNVR 640

QY 339 KKSLEY-----SAISLFNNP 352
DB 641 LLSLYDNHITTTSPGAFDTLQALSTLNLLANP 672
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RESULT 31

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Q8WWZ2          PRELIMINARY;      PRT;    798 AA.
AC Q8WWZ2;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE SLIT1 isoform B (Fragment).
GN SLIT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Teasdale R.D., Rumballe B., Georgas K., Yamada T., Little M.H.;
RA "Conserved modularity, size and potential for alternate splicing in
RT all three human Slit genes".
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029183; AAK31796.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_Out.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00560; LRR; 15.
DR Pfam; PF01463; LRRCT; 3.
DR Pfam; PF01462; LRRNT; 4.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00370; LRR; 11.
DR SMART; SM00082; LRRCT; 3.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_TYP; 16.
FT NON_TER 1
FT NON_TER 798
SQ SEQUENCE 798 AA; 88906 MW; 1A9094A414BABD04 CRC64;

Query Match      16.1%; Score 320; DB 4; Length 798;
Best Local Similarity 24.7%; Pred. No. 1.2e-14;
Matches 100; Conservative 69; Mismatches 124; Indels 112; Gaps 11;

QY 74 CPFGCCQCYSRVHCSDGLTSLVPTNIP----- 100
DB 265 CPAMCTCSNGIVDGRGKLTAFANLPETWETIRLELNGIKSIIPGAFSPYRKLRIPL 324
QY 101 -FDTPLMLDLQNNKIKETKENDFKGLTSLYGLIILNNKLTIKHPKAFITTKKRLRLSHN 159
DB 325 SFCSPCDLSNNQIAETAPDAFQGLRSLNSLVYGNKITTDLPRGVGGLYTLQLLLNAN 384
QY 160 QLSI-----PLNPKSLAELRIHENKVKKIOKDTFKGMNALHVLMSANP----- 205
DB 385 KINCIRPDAFQDLQNLALLSYDNKIQSLAKGTTSLRAIOTLHLAQNPFICDCLKWL 444
QY 206 --LDNNGIE-----PGAFE-----GV 219
DB 445 DFLTNPIETSGARCASPRLANRKGQIKSKKPRCSAKQYPIPETGYQLNSECNSDV 504
QY 220 TVFH-----TRIAEAKLTSVPKGLPPTLLHLHDYNNKISTVELED-FKRYKELQRLG 270
DB 505 VCPHKRCLEANVVCSSSLKTKIPERIPQSTAEALRNNEISILEATGMFKKLTLLKKIN 564
QY 271 LGNNKITYDIENGSLANTPRVRETHLENNKLUKIPSGL-PELKYLIQIFLHNSIARGVN 329
DB 565 LSNKVKSEIEDGAFEGAAVSSELHNTANQLESIRSGMFRGLDGLRTIMLRNNRISCIH-N 623
QY 330 DFCFTVPEMKKSUYSAISLFPNNPKYWEWOPATFRCVLSRMSVOL 374
DB 624 DSFTGLRNVR-----LLSLYDNOIT--TVSPGAFDTLQSLSTLNL 661

RESULT 32
Q9XYV4
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Q9XYV4          PRELIMINARY;      PRT;    1504 AA.
AC Q9XYV4;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE SLIT protein.
GN SLI OR SLIR OR CG8355.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99200390; PubMed=10102267;
RA Kidd T., Bland K.S., Goodman C.S.;
RT "Slit is the midline repellent for the robo receptor in Drosophila.";
RL Cell 96:785-794(1999).
DR EMBL; AF126540; AAD26567.1; -.
DR HSSP; P00740; IEDM.
DR Flybase; FBgn0003425; sli.
DR InterPro; IPR000152; Asx_Hydroxyl.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_Out.
DR Pfam; PF00007; Cys_knot; 1.
DR Pfam; PF00008; EGF; 7.
DR Pfam; PF00054; laminin_G; 1.
DR Pfam; PF00560; LRR; 17.
DR Pfam; PF01463; LRRCT; 4.
DR Pfam; PF01462; LRRNT; 4.
DR PRINTS; PR00011; EGF_LAMININ.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00001; EGF_Like; 5.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00370; LRR; 4.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_TYP; 9.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_3.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_7.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS01187; EGF_CA; 2.
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SQ SEQUENCE 1504 AA; 168569 MW; A377D3BAACBIC743 CRC64;

Query Match      16.1%; Score 320; DB 5; Length 1504;
Best Local Similarity 25.2%; Pred. No. 2.5e-14;
Matches 105; Conservative 57; Mismatches 124; Indels 130; Gaps 9;

QY 74 CPFGCCQCYSRVHCSDGLTSLVPTNIPDTRMLDQNNKIKETKENDFKGLTSLYGLIN 133
DB 73 CPFCVCTGLNVDCSHRGTLSPVKISADVERLELQGNLTVIVETDQRLTKRLMLQLT 132
QY 134 NKKLTKIHPKAFITTKKRLRLYLSHNLSEIPLNL---PKSLAELRIHENKVKKIQDTP 190
DB 133 DNQHTTIERNSPQDLVLSLERLNNRLKAIPENFVTSSALLRLDTSNNVITTVGRVF 192
QY 191 KGMNALHVLMSANPLDNNGI---EPGAFEGVTVFHI----- 224
DB 193 KGAQSLSLQ-----LDNNQITCLDEHAFKGLVEILTLNANNLTSLPHNIFGLGLRL 247
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DR	PROSITE; PS01225; CTCX_2; 1.
DR	PROSITE; PS00022; EGF_1; UNKNOWN_9.
DR	PROSITE; PS0186; EGF_2; 8.
DR	PROSITE; PS01187; EGF_CA; 2.
KW	Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SQ	SEQUENCE 1530 AA; 167385 MW; 622A510E9ACC9B5F CRC64;

Query Match		16.0%; Score 319; DB 11; Length 1530;
Best Local Similarity		25.0%; Pred. No. 3,le-14;
Matches	98; Conservative	63; Mismatches 117; Indels 114; Gaps 10;

QY	74	CPFGCQCYSRVVHCSDLGLTSVPNPDPDT-----RMLDL 108
		: : : : : : : : : : : :
Dd	282	CPAMCSCSNGVDCRGKLTAPANLP-ETMTEIRLELNGIKSIPPGAFSPYRKLRIDL 340
		: : : : : : : : : : : : :
QY	109	QNKKIKEIKENDFKGLSLYLGIILNNNKLTIHPKAFLTTRKKRLRYLSHNOLSEI---P 165
		: : : : : : : : : : : : : :
Dd	341	SNNOIAETAPOAFGLRSLSNLVLYGNKITDLPGRVFGGLTYQLLLLNANKINCIRPDA 400
		: : : : : : : : : : : : : :
QY	166	LNLPKSLAEALRIHENKVKKIQDKTFKGMAHLVLVMSANP-----LDNNGIE 212
		: : : : : : : : : : : : : : : : : : :
Dd	401	FQDLQNTLSLLSYDNKIQSIAKGTFTSLRAQTLLHAQNPFCDCLKWLADFLRTNP 460
		: : : : : : : : : : : : :
QY	213	-PGA-----FEQTVFH----- 223
Dd	461	TTGARCASPRRLANKRIGQISKSKFRCSAKQYFIPTGTDYHLNSECTSDVACPHKCRC 520
		: : : : : : : : : : : : :
QY	224	--IRIAEAKLTSVPKGLPPTLLHLHDYNKISTVELED-FKRYKELOQLGNGNKITDI 279
		: : : : : : : : : : : : : :
Dd	521	ASVVECSGLKUSKIPERIPQSTTELRLUNNEISILEATGLFKULSHLAKKINLSNKKVSEI 580
		: : : : : : : : : : : : :
QY	280	ENGLSANIPRVREIHLNENKLIKIPSGU-PELKYLIQIFLHSNSTIARYGVNDFCPTVPKM 338
		: : : : : : : : : : : : : :
Dd	581	EDGIFEGATSVELHLTANQLESVRSGMRGLDGLWSLMLNRNISCHNDSFTGLRNVR 640
		: : : : : : : : : : : : : :
QY	339	KKSly-----SAISLFNFP 352
Dd	641	LLSLYDHNHTTISPFAFDTLQAALSTLNLNANP 672
		: : : : : : : : : : : : :

RESULT 34
Q9DE37 PRELIMINARY; PRT; 1515 AA.
ID Q9DE37 AC Q9DE37; 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Slit3.
GN SLIT3.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MICHIGAN;
RA Yeo S.Y., Okamoto H.;
RT "zebrafish slit3 homolog.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF210320; AAG36772.1; -
DR HSSP; P00740; 1EDM.
DR ZFIN; ZDB-GENE-010306-4; slit3.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.


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QY 231 -----LTSVPKGLPPTLLEHLHDYNNKISTVELEDFK 261
Db 269 EPPSCNANSICSPCTCSNNIVDCRCKGLMEIPANLPEGIVIRLEQNSIKAIPAGATT 328
QY 262 RYKELQRLGNGNKKITDIENGSLANIPRVREIHLNENKPKIPSGLPE-LKYLQIIFLHS 320
Db 329 QYKLRIDISKNOISDIAPDAFQGLKTSLSLYGNKITEIAKGLFDGLVSLQILLNA 388
QY 321 NSTARVGVNDFCTVPKMKKSLYSALSFLNNPVK 354
Db 389 NKINCLRVNTF-----QDLQNLNLSLYDNKLO 416

RESULT 36
Q9BGP6 PRELIMINARY; PRT; 581 AA.
AC Q9BGP6;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical 65.9 kDa protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FRONTAL LOBE LEFT;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB056426; BAB33084.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00560; LRR; 9.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_TYP; 9.
DR KW Hypothetical protein.
SQ SEQUENCE 581 AA; 65895 MW; A025CF13AA663730 CRC64;

Query Match 15.3%; Score 304.5; DB 6; Length 581;
Best Local Similarity 28.8%; Pred. No. 1e-13;
Matches 87; Conservative 57; Mismatches 105; Indels 53; Gaps 9;

QY 74 CPFGCQSVRVHCSDLGTSVPTNIPDTRMLDLQNNKKEIKENDFKGLTSLYGLILN 133
Db 34 CPKGCRCGKVMYCESQKLEIPSSISAGCLGLSLRNSLQKLYNQFGLNQLTWLYLD 93
QY 134 NNKLTIKHPKAFITTKLRLRYLSHNLSEIPLNPKSLAELRIHENKVKKIQKDTFGKM 193
Db 94 HNHSIDENAFNGIRRLKELILSSNRISYF-LN-----NTRFV 132

QY 194 NALHVLMSANPLDNGIEPGAFGVTVFHRTAEAKLTSPKGLPPTLLEHLHDYNNKIS 253
Db 133 TNLRLNLSYNQLHSLGSE--QFRGLR-----KLLSLHLSNLSR 170

QY 254 TVELEDFKRYKELQRLGNGNKKITDIENGSLANIPRVREIHLNENKPKIPSGI-PELKY 312
Db 171 TIPVRFQDCRNLELDLGYNRISLRNVFAGMIRLUKELHLHNQFSLNLAFLPRLVS 230
QY 313 LQIIFLHNSIARVGVNDFCTVPKMKKSLYSALSFLNNPVKYMOPATFRCV--LSRM 370
Db 94 HNHSIDENAFNGIRRLKELILSSNRISYF-LN-----NTRFV 132

QY 194 NALHVLMSANPLDNGIEPGAFGVTVFHRTAEAKLTSPKGLPPTLLEHLHDYNNKIS 253
Db 133 TNLRLNLSYNQLHSLGSE--QFRGLR-----KLLSLHLSNLSR 170

QY 254 TVELEDFKRYKELQRLGNGNKKITDIENGSLANIPRVREIHLNENKPKIPSGI-PELKY 312
Db 171 TIPVRFQDCRNLELDLGYNRISLRNVFAGMIRLUKELHLHNQFSLNLAFLPRLVS 230
QY 313 LQIIFLHNSIARVGVNDFCTVPKMKKSLYSALSFLNNPVKYMOPATFRCV--LSRM 370
Db 94 HNHSIDENAFNGIRRLKELILSSNRISYF-LN-----NTRFV 132

QY 194 NALHVLMSANPLDNGIEPGAFGVTVFHRTAEAKLTSPKGLPPTLLEHLHDYNNKIS 253
Db 133 TNLRLNLSYNQLHSLGSE--QFRGLR-----KLLSLHLSNLSR 170

QY 254 TVELEDFKRYKELQRLGNGNKKITDIENGSLANIPRVREIHLNENKPKIPSGI-PELKY 312
Db 171 TIPVRFQDCRNLELDLGYNRISLRNVFAGMIRLUKELHLHNQFSLNLAFLPRLVS 230
QY 313 LQIIFLHNSIARVGVNDFCTVPKMKKSLYSALSFLNNPVKYMOPATFRCV--LSRM 370
Db 94 HNHSIDENAFNGIRRLKELILSSNRISYF-LN-----NTRFV 132
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Db 231 LQNLYLQWNKISVIG-----QTMSTWSSSL-QRLDLSGNEIEAFS-GPSVFCQVNPQLRL 283
QY 371 SV 372
Db 284 NL 285

RESULT 37
Q95KI8 PRELIMINARY; PRT; 581 AA.
AC Q95KI8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Hypothetical 65.9 kDa protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TEMPORAL LOBE RIGHT;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB060846; BAB46868.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR Pfam; PF00560; LRR; 9.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00013; LRRNT; 1.
DR KW Hypothetical protein.
SQ SEQUENCE 581 AA; 65880 MW; 8E4F1BBD043669BF CRC64;

Query Match 15.3%; Score 304.5; DB 6; Length 581;
Best Local Similarity 28.8%; Pred. No. 1e-13;
Matches 87; Conservative 57; Mismatches 105; Indels 53; Gaps 9;

QY 74 CPFGCQSVRVHCSDLGTSVPTNIPDTRMLDLQNNKKEIKENDFKGLTSLYGLILN 133
Db 34 CPKGCRCGKVMYCESQKLEIPSSISAGCLGLSLRNSLQKLYNQFGLNQLTWLYLD 93
QY 134 NNKLTIKHPKAFITTKLRLRYLSHNLSEIPLNPKSLAELRIHENKVKKIQKDTFGKM 193
Db 94 HNHSIDENAFNGIRRLKELILSSNRISYF-LN-----NTRFV 132

QY 194 NALHVLMSANPLDNGIEPGAFGVTVFHRTAEAKLTSPKGLPPTLLEHLHDYNNKIS 253
Db 133 TNLRLNLSYNQLHSLGSE--QFRGLR-----KLLSLHLSNLSR 170

QY 254 TVELEDFKRYKELQRLGNGNKKITDIENGSLANIPRVREIHLNENKPKIPSGI-PELKY 312
Db 171 TIPVRFQDCRNLELDLGYNRISLRNVFAGMIRLUKELHLHNQFSLNLAFLPRLVS 230
QY 313 LQIIFLHNSIARVGVNDFCTVPKMKKSLYSALSFLNNPVKYMOPATFRCV--LSRM 370
Db 231 LQNLYLQWNKISVIG-----QTMSTWSSSL-QRLDLSGNEIEAFS-GPSVFCQVNPQLRL 283

QY 371 SV 372
Db 284 NL 285

RESULT 38
Q8TF66 PRELIMINARY; PRT; 581 AA.
AC Q8TF66;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
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[illegible]

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RESULT 42
Q63156 PRELIMINARY; PRT; 96 AA.
AC O63156;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Decorin (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LUNG;
RA Moats-Staats B.M., Stiles A.D., Xu L.;
RT "Expression of decorin RNA in rat lung undergoing chronic lung
RT injury.";
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: L75825; AAA85371.1; -.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_out.
DR Pfam: PF00560; LRR; 3.
DR SMART: SM00370; LRR; 2.
FT NON_TER 1 1
FT NON_TER 96 96
SQ SEQUENCE 96 AA; 10398 MW; C6D19F1750B050D0 CRC64;

Query Match 14.4%; Score 287; DB 11; Length 96;
Best Local Similarity 54.2%; Pred. No. 2.1e-13;
Matches 52; Conservative 20; Mismatches 24; Indels 0; Gaps 0;

Qy 223 HIRTAEAKLTVPKGLPTLLELHDYNNKISTVELEDFKRYKELQRLGLGNKKTIDENG 282
:||||: :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 VIRIADTNTSIPOGLPPSLTLDHGDKNSKRVDAASTKLGNLNAKLGLSFNISAVDNG 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Ov 283 SIANTPRVRETHLENNKLLKIPSGLPKLYQIOTFL 318

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283 SLANIPRVREIHLNENKLLKIPSG---LPELKYLQIIFLHNSIARVGYNDF 331
      :| : : | | | : | : | : | : | : | : | : | : | : | : |
264 IFMQLPHNKLTLFGNSLKLKELSPGVGPMPIUREL---WLYNNHITSLPDAF 313

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Q9D3K0 PRELIMINARY: PRT: 391 AA.

RESULT	44
Q9Z166	
ID	PRELIMINARY; PRT: 1025 AA.
AC	Q9Z166;
DC	01-MAY-1999 (TrEMBLrel. 10, Created)
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	Neurogenic extracellular slit protein (fragment).
GN	SLIT2.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCBI_TaxID=10090;
RP	(1)
FP	SEQUENCE FROM N.A.

Best Local Similarity	28.3%;	Pred. No. 2.4e-12;	Indels	39;
Matches	83;	Conservative	55;	Mismatches
Matches	116;	Indels	39;	Gaps

DR	SMART; SM00282;	LamG; 1.
DR	SMART; SM00370;	LRR; 1.
DR	SMART; SM00082;	LRRCT; 2.
DR	SMART; SM00013;	LRRNT; 2.
DR	SMART; SM00369;	LRR_TYP; 4.
DR	PROSITE; PS00010;	ASX_HYDROXYL; UNKNOWN_2.
DR	PROSITE; PS01185;	CTCK_1; UNKNOWN_1.
DR	PROSITE; PS01225;	CTCK_2; 1.
DR	PROSITE; PS00022;	EGF_1; UNKNOWN_9.
DR	PROSITE; PS01186;	EGF_2; 7.
DR	PROSITE; PS01187;	EGF_CA; 2.
KW	Calcium-binding; EGF-like domain; Glycoprotein; Repeat.	
FT	NON_TER	1
SQ	SEQUENCE	1025 AA; 112974 MW; 46CD0D5B7246FC72 CRC64;
<hr/>		
Query Match	14.2%;	Score 282.5; DB 11; Length 1025;

Query Match

SQ SEQUENCE 1095 AA; 120689 MW; F6C8B2E483D3A66E CRC64;
 Query Match 14.2%; Score 282; DB 13; Length 1095;
 Best Local Similarity 22.9%; Pred. No. 8.8e-12;
 Matches 89; Conservative 65; Mismatches 132; Indels 102; Gaps 8;

 QY 73 MCPGOCYCYSRVVCHSCDLGLTSVPTNIPFD-----RMLD 107
 :|| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 75 VCPCKRCCEGTVDSCSNOKLRLPSHLPEVTTLRLNDNDISVL EATGLFKLPNLRKIN 134
 :|| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 QY 108 LONNKIKEIKENDPKGLTSLYLNNKLTTHPAFLTKKLRLLYLSHNSOLSEPLN 167
 :||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 135 LSNKKIKEIREGTFDGASGVQEOELITNQUESVHGFRGLTGKTLMLRSNISCIIND 194
 :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 QY 168 LPKSLABEL---IHENKVKKIQDKTFKGMAHALHVLEMSANPDNN----- 209
 :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 195 TFAGLSVRLLSLDYDNHSITTPCAFSTLYSLSTINLLANSFNCNCHLAWLGWLRKKRI 254
 :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 QY 210 -----GIEGAFEGTVVFH-----TRIAEAKL 231
 :|| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 255 VSGNPRLCKPFFLKDIPIQDVDAQDFTCGNDESSCLLPPCPSQCTCVDSVVVRCNSKGL 314
 :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 QY 232 TSPVKGPUPPLLHLHDYNKSIVLELDFKRYKELQRLGNGKNKITDIENGSLANIPRV 291
 :||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 315 RVMPKGI PKDVTLEYLEGNHLTAV -KLSAFRLHTLIDLSNNSISVLANTFSNNTQLS 373
 :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 QY 292 EIHLNNKKKKIP-SGLPELKYLIQIFLHNSIARYGVNDFCTPMKKSKLSAISLFN 350
 :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 374 TLILSYNRLRCIPVHAFGNLSRLSVLTLCGNDISSVPEGSFNDLV-----LSHLALGT 427
 :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 QY 351 NP-----VKYWEMQPATPRC 365
 :|| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 428 NPLHCDCNRLSEWVKAGYKEPGIARC 455

 RESULT 46
 Q8R5M3 PRELIMINARY; PRT; 578 AA.
 ID Q8R5M3
 AC Q8R5M3;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Lib.
 GN RLIB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;
 OC NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WISTAR RATS; TISSUE=BRAIN;
 RX MEDLINE=21645900; PubMed=11785964;
 RA Satoh K., Hata M., Yokota H.;
 RT "A Novel Member of the Leucine-Rich Repeat Superfamily Induced in Rat
 RT Astrocytes by beta-Amyloid";
 RL Biochem. Biophys. Res. Commun. 290:756-762(2002).
 DR EMBL; AB071036; BAB84586.1; -.
 SQ SEQUENCE 578 AA; 64127 MW; 991BD057F5912591 CRC64;

 Query Match 14.1%; Score 281.5; DB 11; Length 578;
 Best Local Similarity 27.8%; Pred. No. 4.4e-12;
 Matches 82; Conservative 57; Mismatches 113; Indels 43; Gaps 9;

 QY 74 CPGGCOCYSRV--VHCSDLGLTSVPTNIPFTDRMLDLQNKKIKEIKENDPKGLTSLYGLI 131
 :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 25 CPSECTC-SRASOECTGARIVAMPTPLPNAMSLOVVVTHTELPENFLNLSIALALK 83
 :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 QY 132 LNNKLTTHPAFLTKKLRLLYLSHNSOLSEPL-----NLP----- 169
 :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 84 MEKNELSTIMPGAFRNLGSLRSLSLANNKLRLPIRVQDVNNLESLLLSNNOVQIOQA 143
 :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 QY 170 ----KSLAEFLRHENKVKKIQDKTFKGMAHALHVLEMSANPDNNNGIEPGAEGTVVFH 224
 :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 144 QFSQSNRLRELQHGNNLESIPEAFDHLVGLTKLNLGRNSFTH--LSPRLFQHLGNLQV 201
Q9N4G6
QY 225 -RIAEAKTSPKPG--LPPTLLLEHLDYNNKISTVELEDFKRYKELQRLGLGNKKITDIE 280
Db 202 LRLHENRUSDIPMGFTFALGNLQALQEOIGTSLPGLFHNNKRLQRLYLSNNHISQLP 261
QY 281 NCSLANIPRVREIHLNNKLLKIPSG---LPELKYLIQIIFLNSNSIARVGVNDF 331
Db 262 PGIFMQLPOLNKLTLFGNSLRELSPGVFGMPNPLREL--WLYNNHTSLADNTF 313

RESULT 47
Q9N4G6 PRELIMINARY; PRT; 542 AA.
AC Q9N4G6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Y71F9B.8 protein (ID304).
GN Y71F9B.8 OR ID304.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN None;
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL science 282:2012-2018(1998).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Kohara Y., Shin'i T., Suzuki Y., Sugano S., Potdevin M.,
RA Thierry-Mieg Y., Thierry-Mieg D., Thierry-Mieg J.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC024201; AAF36020.1; -.
DR EMBL; AF304125; AAG50238.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF01463; LRRCT; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00370; LRR; 5.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_TYP; 3.
SQ SEQUENCE 542 AA; 59272 MW; EA5CA06808ADE92E CRC64;

Query Match 14.18; Score 281; DB 5; Length 542;
Best Local Similarity 26.5%; Pred. No. 4.9e-12;
Matches 90; Conservative 61; Mismatches 122; Indels 66; Gaps 10;

QY 74 CPGCGQYSRVVH-CSDGLGTSVPTNIPDFDRMLDLONNKTKETKENDFKGLTSLYLIL 132
Db 18 COSGCKPRTKTAVCCKGSSLSRIPILDPRTTVLDLSNNRISRLSADLSLYPLNEQLIL 77
QY 133 NNNKLTIKHPKAFUTTKRLRLYLSHNLSEIP---LNLPSKSLAELRIHKNKVKIKQDT 189
Db 78 HNSHTLSADVFSTPLSLRLVLDLSSNLSLLPLNEVFSKLNKLTLLTSSNDV-QLGPEC 136
QY 190 FKGMAHLVLEMSANPLDNNNGIERGAFEGVT-VFHIRTAELKTVPKGLPPTL--LE-L 245
Db 137 FAGUSQQLTSLADNRL--SFLPPSVLKLPLSLGLRLDLANKLLSMPASVMMNLGGLETL 194

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QY 246 HLDYNNKISTVELEDFKRYKELQRLGLGNKKITDIEGNSLANIPRVREIHLNNKLLKIP- 304
Db 195 KLQNQLSSLETGMLFSOKELHLDVSENIGDIEGALYGLEKLETLNLTNNQLVRPG 254
QY 305 -----SGLPELKYLIQI-----I 316
Db 255 NTWSLPALKTLTDLSSNLFVSLFETASFDGLPALQYLNSHSRLNKTOMATFVOLSLSHL 314
QY 317 FLHNSIARVGVNDFCPTVPKMKKSLYSAISLFLNPNVKY 355
Db 315 SISSSALTHIHPSAFNPIPP-----LSHLDLSNNELRY 347

RESULT 48
Q9VFP0 PRELIMINARY; PRT; 1513 AA.
ID Q9VFP0;
AC Q9VFP0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CG5195 protein.
GN CG5195.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Randell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazef R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Brill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA De Carlos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swierkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AF003591; AAF51605.1; -.
DR FlyBase; FBgn0036995; CG5195.
DR InterPro; IPR002064; DNA_pol_B.

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DR	SMART; SM00370;	LRR; 5.
DR	SMART; SM00082;	LRRCT; 1.
DR	SMART; SM00013;	LRRNT; 1.
DR	SMART; SM00369;	LRR_TYP; 9.
SQ	SEQUENCE	603 AA; 66924 MW; 9E8DEC7A9A2315FF CRC64;

Query Match		13.9%;	Score	276;	DB	11;	Length	603;
Best Local Similarity		28.2%;	Pred No.	1.2e-11;				
Matches	90;	Conservative	58;	Mismatches	107;	Indels	64;	Gaps

QY	102	DTRMLDQNKKIKEIKENDPKGTSILYGLLNKNNKLTKIHPKAFLTTKRLRRLYLHNQL	161
Db	219	ELREDLSRNALRSVANFVHLPRQKLYLDORNLITAVAPRAFLCMKALRWLDSLHNRV	278
QY	162	SEI-----PLN-----PKS-----LAELRIHENKVKKTKDKFKGMN	194
Db	279	AGLMEDTFPGLGLHLVRHAHNAIASLRPTKDUHFLEELQGHNRIRIQLGERTFEGLG	338
QY	195	ALHVLEMSANPLDNNGIEPGAEGTVVFHIRIAEAK---LTSVP---KGLPPTTLELHL	247
Db	339	QLEVTLNDNQITE--VRVGAFSG--LENVAVMNLSGNCLSLPERVFGQL-DKLHSLSL	393
QY	248	DYNKISTVELEDPKRYKELQRGLCGLNKNKITDIENGLANIIPRVRIHLENKCLKIP---	304
Db	394	EESCLGHVRLHTFAGUGLLRUFLRDNSSTSSIEQSAGLSLELDTLTRLTHLPQL	453
QY	305	-SGPELKYLQIIIFLHNSNIARGVNDFCPT-----VPMKMKSYSA-----	345
Db	454	FQGLGHLEYL---LLSYNQLTILSAEVGLPQRAFWDISHNHLETLAGLFSSLGRLRY	510
QY	346	ISLFNPVKYWEMQPATFR	364
Db	511	LSLRNNSLQTFSPPQGLER	529

RESULT	50
Q96DNI	
ID	Q96DNI PRELIMINARY; PRT; 522 AA.
AC	Q96DNI;
CD	01-DEC-2001 (TrEMBLrel. 19, Created)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE	CNA FLJ32082 fis, clone OCBBF2000231, weakly similar to phospholipase
DE	A2 inhibitor subunit B precursor.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID	9606;
RN	[1]
RC	SEQUENCE FROM N.A.
KC	TISSUE=BRAIN;
RA	Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA	Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA	Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA	Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA	Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA	Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H.,
RA	Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA	Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA	Isorai T.;
RT	"NEO Human cDNA sequencing project.";
RL	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RL	EMBL; AK056644; BAB71240.1; -.
DR	InterPro; IPR001611; LRR.
DR	InterPro; IPR000372; LRR_Nterm.
DR	Pfam; PF00560; LRR; 9.
DR	Pfam; PF01462; LRRNT; 1.
DR	SMART; SM00013; LRRNT; 1.
SQ	SEQUENCE 522 AA; 58628 MW; 73000472E124245C CRC64;

Query Match		13.8%;	Score	275;	DB	4;	Length	522;
Best Local Similarity		26.8%;	Pred. No.	1.1e-11;				
Matches	84;	Conservative	54;	Mismatches	115;	Indels	60;	Gaps

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QY 68 FDLPMCPFG----CQYRVVHCSDGLTSVPTNIPEDTRMLDLQNNKIKEIKENDFKG 123
Db 29 FOMLPAAFGCPQLCRCEGRLLYCEALNLTEAPHNLIS-GLGLSLRYNSLSLSELRAGQFTG 87
QY 124 LTSYGLILNKKTKIHPKAFLTTKLRLRLLYLSHNOLSEIPLNPKSLAEELRIHENKVK 183
Db 88 LMQLTWLYLDHNHICSVQGDFAFKLRRVKELTSSNQITQLP----- 129
QY 184 KIQDFTFKCMALHVLMSANPLDNNNGIEPGAFEGVTVFHIRIAFAKLTSPKGLPTLL 243
Db 130 ---NTFRPMNLRSDLSYNKL--QALAPDLFHGL-----RKLT----- 165
QY 244 ELHLDYNNKISTVELEDFKRYKELQRLGLGNKKITDIENGSLANIPRVREIHLNKKLKI 303
Db 166 -LHMFAANAIQFVPVRFODCRSLKFLDIDIGYNQLKSLARNSFAGLFKLTLEHNDLVKV 224
QY 304 P-SGLPELKYLIQIFLHNSIARGVN-DFCPTVPKMKKSLSAISLFNPNVYKWEQPA 361
Db 225 NFAHFPRLISLHSLCLRRNKVAIVVSSLDWVWNLKEM-----DLSGNEIEY--MEPH 274
QY 362 TFRCVLSRMSVOL 374
Db 275 VEETVPHLQSLQL 287

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Search completed: January 24, 2003, 12:26:42
Job time : 46 secs